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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB
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and is derived
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seq length:
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derived by a
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Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hits satisfying chosen parameters:
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(SIDSB/gcgdata/geneseq/yeneseqp/AA199).DAT:*

(SIDSB/gcgdata/geneseq/geneseqp/AA199).DAT:*

(SIDSB/gcgdata/geneseq/geneseqp/AA2000.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A_Geneseq_1101:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         522463 seqs, 74073290 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
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2292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MVPEPGPTANSTPAWGAGPP.....FNIDPAEPELRPHPLGIPTN 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDSB/gcgdata/geneseq/geneseqp/AA1984.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1986.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1987.DAT:*
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                                437
477
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                  AAR36801
AAB70765
AAW44933
AAR32501
AAR26505
AAR62515
AAR62515
AAR713737
AAR54992
AAR15498
                                                                                                                                                                                                                                                                SUMMARIES
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1314.204 Million cell updates/sec
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                                               Adrenalin receptor Bovine beta3 adren Murine beta-1 adre Murine beta-3 adre
                                                                                                                                                                                                           Description
              Human dopamine D1 Human dopamine D1
                                                                                                                   Beta-adrenergic re
                                                                                                                                     Human betal-adreno
Canine beta-3 adre
                                                                                                                                                                          Rat serotonin St-B
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	AAW02665	17	377	21.0	481.5	٠,
	AAR48693	15	377	21.0	481.5	_
Rat alpha-1b adren	AAB59667	22	515	•	484	w
Human adrenorecept	AAU05408	22	515	•	485.5	١٠
Human alpha-1alpha	AAB59665	22	501	21.2	485.5	_
Mouse alpha-1b adr	AAY67236	21	515	•	486	_
opamine	AAR31046	14	475	•	487.5	•
	AAR90041	16	515		488	w
rt	AAR70995	15	515	•	488	7
	AAW40802	18	477	21.3	488	٠,
rec	AAR79381	16	477	21.3	488	01
Sequence of human	AAR52830	15	572	21.4	489.5	-
oha-	AAR90040	16	501	21.4	491.5	w
Dopamine D1 recept	AAR21082	13	477	21.4	491.5	١٥
Hamster alpha-1b a	AAB59668	22	515		493	_
onir	AAB45805	22	478	•	494.5	_
orm	AAY28853	20	478	21.6	494.5	•
nce of Hul	AAY57168	21	501		499.5	w
alpha-1A	AAR70996	15	501	•	499.5	~
alpha-1A	AAR58681	15	572		500	٠,
alpha-	AAB59662	22	572	•	503	٠.
-	AAR98563	17	572	21.9	503	_
-1A adren	AAR85945	16	572	•	503	w.
alpha-1A ad	AAR90039	16	572	21.9	503	
	AAR53071	15	572	•	503	_
n adrenor	AAU05409	22	565	22.0	503.5	_
	AAB59666	22	560	•	507.5	•
-	AAW33185	18	379	•	508	w
H	AAR13596	12	487	•	527.5	7
beta-3 adre	AAR54991	15	408	•	531	٠,
ρ	AAW53847	19	407	•	531	٠.
ergi	AAR06495	11	402	•	531	_
t dopamine	9	12	446	23.2	531.5	w
D1 dopamine recept	AAW09795	18	487	•	533.5	٠

## ALIGNMENTS

AAR36801 RESULT

AAR36801 standard; Protein; 437

AA

25-AUG-1993 AAR36801;

(first entry)

Rat serotonin St-B17 receptor

Cloned gene encoding serotonin St-B17 receptor gene test drugs for CNS activity 01-APR-1993 Polymerase chain reaction; primer; PCR; amplify; rat; serotonin; g-protein; receptor; catecholamine; St-B17; St-B17; drug; CNS; intron; splice; clone; transmembrane; 5-HT; family; hydrophobic; 5-HT2; 5-HT1D; 5-HT1B; 5-HT1A; 5-HT1E. WPI; 1993-159491/19. N-PSDB; AAQ41701-2. 26-OCT-1992; 26-OCT-1992; US7970338-A. Synthetic. Monsma FJ, (USSH ) US DEPT HEALTH & HUMAN SERVICE. Sibley DR; 92US-0970338 9205-0970338 used 5

Murine adrenergic

by the

encodes

encodes the rat serotonin St-B173 receptor and was clone St-B173. The putative intron, found in clo

clone

Page

51pp; English.

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RESULT
AAB70765
ID AAB7
XX
AC AAB7
XX
DT 18-P
XX
DE Human
XX
KW Beta
XX
KW Carr
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   St-B172, was absent from this clone with the flanking exons being spliced together at nucleotide 873. Splicing at this position results in a 1311 bp open reading frame encoding a protein of 437 amino acids with a molecular weight of 46.8 kb. Hydropathy analysis of this amino acid sequence indicated several hydrophobic regions predicted to
              cardiomyopathy;
                              Betal-adrenoreceptor; human; mutation;
                                                             Human betal-adrenoreceptor
                                                                                             18-MAY-2001
                                                                                                                                                        AAB70765 standard; Protein;
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                                                                                                                                                                                                                                                                                                              SHSGPRPGLSLQQVLPLPLPDSDSDSDSDSDSGSGGSSGLRLTAQLLLPGEATQDPPLPTRAA 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  candidates.
                                                                                                                                                                                                                                                                   AAVNFFNIDPAEPELRPHPLGIPTN 440
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                                                                                                                                                                                                                                                                                                                                                                                                                      \tt rtprpgmesadsrrlatkhsrkalkasltlgillgmffvtwlpffvaniaqavcdcispg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mvpepgpvnsstpawgpgpppapggsgwvaaalcvvivltaaansllivlictqpavrnt 60
                                                                                                                                                                                                                                                                                              qrcqtrp--qlqqvlalplppnsdsds--asggtsglqltaqlllpgeatrdpppptrat
                                                                                                                                                                                                                                                                                                                                                            lldvltwlgycnstmnpiiyplfmrdfkralgrflhastvpr----stgqpclplhvdls
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                                                                                                                                                                                                                                                                                                                                                                                                                                        375;
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                                                                                          (first entry)
                 dilative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.6%;
84.3%;
                                                               protein
                                                                                                                                                           477
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Pred. No. 8.2e-176;
Pred. No. 8.2e-176;
                                disease predisposition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 14; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 13;
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20 В δÃ

ALGRELPCPR---CPRERQASLASPSLRTSHSGPRPGLS--LQQVLPLPLP-PDSDSDSDSD

383 385 329

272

212 176

mgvftlcwlpfflanvvkafhrelvpdrlfvffnwlgyansafnpijycrsp----dfrk LGMEFYTWLPEFYANIYQAY-CDCISPGLFDVLTWLGYCNSTMNPIIY---PLFMRDFKR

274

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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 that comprises 1-70 or more mutations, excluding the sequence with the comprises 1-70 or more mutations, excluding the sequence with the comparison shala45Gly or Gly1165Cys. The invention also describes (1) can method for determining predisposition to disease by genotyping DNA of CC (1) at one or more exchanged position and comparison with a reference conclude at least one of the amino acid changes Ser49Gly, Ala59Ser, CC include at least one of the amino acid changes Ser49Gly, Ala59Ser, CC Gly389Arg, Arg399Cys, His402Arg, Thr404Ala and/or Pro418Ala, but CC excluding the sequence with a single amino acid exchange at positions 49 CC or 389. Genotyping of (1) is used to determine predisposition to CC cardiomyopathy, specifically the dilative form, also for prognosis and CC assessing severity of this condition. Gene (1) can be used for the CC of beta1-adrenoreceptor (ant)agonists; (ii) construction of genes or CC vectors, especially for pharmaceutical development; specifically a new class conditional responses to different beta1 adrenoreceptor, (ant)agonists, (iii) construction and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wallukat G,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-AUG-1999;
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pspspspvpapapppppppaaaaataplangragkrrpsrlvalreqkalk---tlgii
                                                                      ASET-----
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                                                                                                                                                                                                            PGQCRLLASLPFVLVASGLTFFLPSGAICFTYCRILLAARKQAVQVAS----LTTGMASQ
                                                                                                                                                                                                                                                                                                                                                            SLDRYLLILSPLRYKLRMTPLRALALVLGAWSLAALASFLPLLLGW--HELGHARPPV--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           predisposition to develop side effects and habituation.
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                                                                      LQVPRTPRPGVESADS------RRLATKHSRKALKAKLTLGIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 561; DB 22;
Pred. No. 4.6e-46;
6; Mismatches 161;
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14;

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This sequence represent the canine beta 3-adrenergic receptor (RA-Ca-b3). The coding sequence was isolated from a cDNA library constructed from polyA+ RNA purified from dog brown adipose tissue cells. The probe was a fragment of the coding region of the human beta-3 adrenergic receptor covering the region from the initiation codon to transmembrane domain 7 (TM7) amplified by primers AAV30511-V30512. The full length insert was cloned into M13 for sequencing using primers AAV30470-V30490. The sequence can then be expressed e.g. in a mammalian cell, by subcloning into an expression vector such as pCDNA3. RA-Ca-b3 has been implicated in obesity and obesity-related metabolic disorders
                                                                                                                               Canine beta 2 and beta 3 adrenergic receptors and coding useful for identifying specific ligands and (ant)agonists specific treatments for obesity in dogs
                                                                                                                                                                        WPI; 1998-032136/03.
N-PSDB; AAV30469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canis familiaris.
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                                                                                                              Claim 3;
                                                                                                                                                                                                    Drumare MF,
                                                                                                                                                                                                                        (VETI-) VETIGEN
                                                                                                                                                                                                                                          26-MAR-1996;
                                                                                                                                                                                                                                                             26-MAR-1997;
                                                                                                                                                                                                                                                                                 02-OCT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW44933;
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                                                                                                                                                                                                                                                                                                                                                                      Domain
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AAR32501
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e.g. diabetes. The canine version of RA-Ca-b3 can be used to develop treatments specific for dogs. The sequence can also be used in differential screening for ligands for RA-Ca-b3 as compared to the betadrenergic receptor (AAW44932).
Fat cell specific beta- adrenergic receptor polypeptide - used for diagnosis of obesity due to inactive lipolysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-JUN-1993
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                                                                                                                                                                               01-NOV-1991;
                                                                                                                                                                                                                                                                                                                                      Rattus rattus
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                                                                                                  Venter
                                                                                                                                    (USSH ) US DEPT HEALTH & HUMAN SERVICE
                                                                                                                                                                                                                                                                                                                                                                             thermogenesis;
                                                                                                                                                                                                                                                                                                                                                                                               Fat cell specific; BAR; lipolysis; obesity; diagnosis;
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                                                           1993-067426/08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ETLQVPRTPRPG------VESADSR--RLATKHSRKALKAKLTLGILLGMFFVTWL
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                                                                                                                                                                                                                                                                                                                                                                               metabolism.
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Pred. No. 6.5e-46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probes with DNA probes encoding human beta-1 and rat beta-2 adrenergic receptors under low stringency conditions. Positive clones were found to be different from the rat and human sequences and contained a single open reading frame of 1200 bp encoding the protein shown, of 400 amino acids and mol. wt. 43 kD. The protein is the fat specific beta-adrenergic receptor and may be used in work on the thermogenesis process. Isolation of the gene for BAR allows the diagnosis and treatment of obesity and the testing of medications for their effectiveness in stimulating the thermogenesis metabolic
                                       15-FEB-1991;
                                                                     03-AUG-1992.
                                                                                              JP04211374-A
                                                                                                                          Rattus rattus
                                                                                                                                                                   Drugs; dubutamine;
                                                                                                                                                                                               Adrenalin
                                                                                                                                                                                                                           12-FEB-1993
                                                                                                                                                                                                                                                                                 AAR26505 standard; Protein; 466
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           27-FEB-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       LGMFFVTWLPFFVANIVQAVC--DCISPGLFDVLTWLGYCNSTMNPIIY---PLFMRDFK 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   elgpatveesprspsrspspatvgtptasdgvpscgrrparllplgehralr---tlgli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTGMASQASETLQVPRTPRP------GVESADSR--RLATKHSRKALKAKLTLGIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LNLCLISLDRYLLILSPLRYKLRMTPLRALALVLGAWSLAALASFLPLLLGWHELG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PALRNTSNFFLVSLFTSDLMVGLVVMPPAMLNALYGRWVLARGLCLLWTAFDVMCCSASI
                                                                                                                                                                                                                                                                                                                                                                               RAL----GRFLPCPRC---PRERQASLASPSLR--TSHSGPRP
                                                                                                                                                                                                                                                                                                                                                                                                             mgifslcwlpfflanvlralvgpslvpsgvfialnwlgyansafnpliycrspdfrdafr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pwphkngslafwsdaptldpsaantsglpgvpwaaalagallalatvggnllvitaiart 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGPTANSTPA-WGAGP---PSAPGGSG-----WVAAALCVVIAL-TAAANSLLIALICTQ 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in obesity patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          400 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                         (first entry)
             90JP-0048794
                                         91JP-0044479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                   prenalterol; acebutolol; metoprolol;
                                                                                                                                                                                             subtype beta-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 557.5; DB 14;
; Pred. No. 8e-46;
61; Mismatches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English
                                                                                                                                                                                                                                                                                   A
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RESULT
AAR62515
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding adrenalin receptor sub-type beta-1 - obtd. by cloning rat genome DNA library and rat cDNA library with derived from human adrenalin
Region
            Key
                                      Bos taurus
                                                                            bovine;
                                                                                                      Bovine beta3 adrenergic receptor.
                                                                                                                                06-JUL-1995
                                                                                                                                                            AAR62515;
                                                                                                                                                                                     AAR62515 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1992-304939/37
                                                                 antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SUMU ) SUMITOMO SEIYAKU
                                                                                                                                                                                                                                                      438
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                                                                                                                                                                                                                                                                                --SGGSSGLRLTAQLLLPG
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                                                                                                                                                                                                                                                                                                                                                                                    NIVQAV-CDCISPGLEDVLTWLGYCNSTMNPIIY---PLEMRDFKRALGRELPCPR----C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRLLASLPFVLVASGLTFFLPSGAICFTYCRILLAARKQAVQVASLTTGMAS-----QAS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rylgrtspfryqslltrararalvctvcaisalvsflpilmhwwraesdearrcyndpkc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RYLLILSPLRYKLRMTPLRALALVLGAWSLAALASFLPLLLGW--HELGHARPPV--PGQ 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fimslasadlvmgllvvpfgativvwgrweygsffcelwtsvdvlcvtdsietlcviald, 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FLVSLFTSDLMVGLVVMPPAMLNALYGRWVLARGLCLLWTAFDVMCCSASILNLCLISLD 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ppasllppaseg--saplsqqwtagmglllalivllivvgnvlvivaiaktprlqtltnl 95
                                                                                                                                                                                                                                                                                                                                                                                                                                          ETLQVPRTPRPGVESADSR-----RLATKHSRKALKAKLTLGILLGMFFVTWLPFFVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cdfvtnrayaiassvvsfyvplcimafvylrvfreaqkqvkkidscerrflsgpprppsp
                                                                                                                                                                                                                                                                                                        rr----raahgdrprasaclaragpppspgapsddddddagatpparllepwa
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                                                               beta3 adrenergic ist; regulate fat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is useful in studies of drugs acting on adrenalin class beta 1, e.g. dobutamine or prenalterol, or drucceptor, e.g. acebutolol, metoprolol, atenolol or
                                                                                                                                (first
Location/Qualifiers 38..63
                                                                                                                                                                                      Protein;
                                                                                                                                entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.3%;
                                                               receptor; identification; ac
level; improve meat quality
                                                                                                                                                                                                                                                      456
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                                                                                                                                                                                      405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 557.5; DB 13; Pred. No. 9.7e-46; 3; Mismatches 163;
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                                                                             agonist;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                   AAR62515 shows the amino acid sequence of the bovine beta3 adrenergic receptor encoded by AAQ74367. The peptide contains 7 transmembrane regions, all of which are claimed individually and are useful for the generation of probes for screening compounds that have agonist/antagonist activity to the receptor. (See AAR70668-74). These probes are specific to the beta3 gene and not to beta1 or beta2 genes. These cpds. could be used to regulate the level of fat in animals, partic. for improved meat quality.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid encoding the bovine beta3 adrenergic receptor - are related peptide(s), vectors and transformed cells, useful for identifying specific agonists and antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 16; Page 3.-5; 52pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1994-341770/42.
N-PSDB; AAQ74367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-OCT-1994
                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                 Local Similarity
nes 143; Conserv
                                                                                                                                                                                                                                                  1 MVPEPG-PTANSTPAWGAGPPSAPGGSGWVAAALCVVIALTAAANSLLIALICTQPALRN 59
                                                                                                                                                                          ltpwpdiptlapntanasglpgvpwavalagallalavlatvggnllvivaiartprlqt 70
TWLPFFVANIVQAV -- CDCISPGLEDVLTWLGYCNSTMNPIIY -- -PLFMRDFKRALGRF
                                                                                                                                                                                                     TSNFFLVSLFTSDLMVGLVVMPPAMLNALYGRWVLARGLCLLWTAFDVMCCSASILNLCL 119
                                                                       snprc---ctfasnmpyallsssvsfylpllvmlfvyarvfvvatrq-lrllrrelgrfp
                       peesppapsrsgspglagpcaspagvpsygrrparllplrehralr---tlglimgtftl
                                                                                      ARPPVPGQCRLLASLPFVLVASGLTFFLPSGAICFTYCRILLAARKQAVQVASLTTGM--: | | :::| ::: | ::: |
                                                                                                                          {\tt lavdrylavtnplrygalvtkrralaavvlvwvvsaavsfapimskwwrigadaeaqrch}
                                                                                                                                                  ISLDRYLLILSPLRYKLRMTPLRALALVLGAWSLAALASFLPLLLGWHELG------H 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VETIGEN.
                                                                                                                                                                                                                                                                                                                                                 405 AA;
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                                                 ASQASETLOVPRTPRPGVESADSR--RLATKHSRKALKAKLTLGILLGMFFV
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293..314
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203..26
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/note "transmembrane region 2 (TM2); see AAR70669" 110.131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          French.
                                                                                                                                                                                                                                                                                 61;
                                                                                                                                                                                                                                                                                 Score 554; DB 15;
Pred. No. 1.8e-45;
1; Mismatches 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         region 7 (TM1);
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                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                 Matches 137;
                                                                                                                                                                                                                                                                                           The invention relates to a human amine receptor polypeptide. Host cells transformed with a vector comprising the amine receptor coding sequence are used for the recombinant production of the polypeptide. The polypeptides are useful for treating conditions related to underexpression and over-expression of the human amine receptor. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus
                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 2; 22pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-429497/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murine beta-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY13737;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY13737 standard; Protein; 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN
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  187
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                                               PTANSTPAWGAGPPSAPGGSGWVAA----ALCVVIALTAAANSLLIALICTQPALRNTSNF 63
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\verb|cdfvtnrayaiassvvsfyvplcimafvylrvfreaqkqvkkidscerrflggparppsp|
                         CRLLASLPFVLVASGLTFFLPSGAICFTYCRILLAARKQAVQVAS----LTTGMASQAS- 234
                                                                                                                        FLVSLFTSDLMVGLVVMPPAMLNALYGRWVLARGLCLLWTAFDVMCCSAS1LNLCLISLD 123
                                                                                                                                                ppasllppaseg--saplsqqwtagmgllvalivllivvgnvlvivaiaktprlqtltnl 66
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                                                                                                 fimslasadlvmgllvvpfgativvwgrweygsffcelwtsvdvlcvtasietlcviald 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amine
                                                                                                                                                                                                                                                                                   represents a murine beta-1 adreno-receptor
                                                                                                                                                                                                                                                             365
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                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                              receptor polynucleotides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor; recombinant; murine; beta-1 adreno-receptor
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                                                                                                                                                                                              24.1%; Score 553.5; DB 20; 37.8%; Pred. No. 1.7e-45; tive 56; Mismatches 134;
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Best Local S
Matches 141
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                                                                                                                                                                                                                                                                                                                        Isolated receptor
                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-1992;
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                                                                                                                                                                                                                                                                                     Claim 2; Figure 4; 15pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP600136-A.
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                                                                                                                                Local Similarity 35.1 nes 141; Conservative
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LNLCLISLDRYLLILSPLRYKLRMTPLRALALVLGAWSLAALASFLPLLLGWHELG----
                                                                                                PGPTANSTPA-WGAGP---PSAPGGSG-----WVAAALCVVIAL-TAAANSLLIALICTQ 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nvvkafhrdlvpdrlfvffnwlgyansafnpilycrsp----dfrkafqrllccarraac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ETLQVPRTPRPGVESADSR------RLATKHSRKALKAKLTLGILLGMFFVTWLPFFVA
                                                                                 pwphrngslalwsdaptldpsaantsglpgvpwaaalagallalatvggnllviiaiart 62
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                                                                                                                                                                                                                                                                                                                       and purified polypeptides having beta3-adrenergic activity - are used to study the effects of various
                                                                                                                                                                                                                                                                                                             agents on
                                                                                                                                                                                                                                                                                                                                                                                             Nahmias-kaminski
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                adrenergic receptor
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                                                                                                                                                                                                                                                                                                             the beta3-adrenergic receptor
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                                                                                                                                            24.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                    SCI.
                                                                                                                                 60;
                                                                                                                                Score 552.5; DB 1
Pred. No. 2.4e-45;
0; Mismatches 150
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28-NOV-1991.

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; Protein; 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G-protein-coupled receptor; neurotransmitter; se stimulation.
                                                                                                                                                           /label= transmembrane
/note= "VI"
311..337
                           /label= Protein_kinase_A_phosphorylation_site
/note= "putative"
                                                                           /label= Protein_kinase_A_phosphorylation_site
/note= "putative"
                                                                                                             265..268
                                                                                                                                                                                                                                                                                                                                                           /label- transmembrane
/note= "II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
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                                                                                                                          /note= "VII"
                                                                                                                                          /label= transmembrane
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/note= "IV"
                                                                                                                                                                                                                                                                                                    138..164
                                                                                                                                                                                                                                                                                                                                                                                                         note= "I"
                                                                                                                                                                                                                                                                                                                                                                                                                           /label= transmembrane
                                                                                                                                                                                                                       /label= transmembrane
/note= "V"
                                                                                                                                                                                                                                                                                                                 /label= transmembrane
/note= "III"
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RESULT 1
AAR38364
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cloned gene encoding screening, diagnosis or in gene therapy
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(UYOR-)
AAR38364 standard; Protein; 446
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Dearry A,
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14-MAY-1990;
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les 143; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
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                                                                                                                                                                                sgetqpfcidsntfdvfvwfgwansslnpiiy-afnadfrkafstllgcyrlcpatnnai
                                                                                                                                                                                               -----CISPGLFDVLTWLGYCNSTMNPIIYPLFMRDFKRALGRFLPCPR-CPRERQA-
                                                                                                                                                                                                                                    tttgngkpvecsqpessfkmsfkretkvlk---tlsvimgvfvccwlpffilncilpfcg
                                                                                                                                                                                                                                                    TLQVPRTPRPGVESADSRRLATKHSRKALKAKLTLGILLGMFFVTWLPFFVANIVQAVCD
                                                                                                                                                                                                                                                                                          idncdsslsrtyaisssvisfyipvaimivtytriyriaqkqirriaaleraavhakncq
                                                                                                                                                                                                                                                                                                                     --QCRLLASLPFVLVASGLTFFLPSGAICFTYCRILLAARKQAVQVASL-TTGMASQASE
                                                                                                                                                                                                                                                                                                                                                                            LSPLRYKLRMTPLRALALVLGAWSLAALASFLPLLLGWHELGHARPPVPG------
                                                                                                                                                                                                                                                                                                                                                                                                                                   FTSDLMVGLVVMPPAMLNALYGRWVLARGLCLLWTAFDVMCCSASILNLCLISLDRYLLI 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                               samdgtglvverdfsvriltacflsllilstllgntlvcaavirfrhlrskvtnffvisl 66
                                                                                               GEATQDPPLPTRAAAAVNFFNIDPAEPELRP-----
                                                                                                                         etvsinnngaamfsshheprgsiskecnlvyliphavgssedlkkeeaagiarpleklsp
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OREGON HEALTH SCI UNIV
                                                                                                                                                     -SLASPSLRTSHSGPRPGLSLQQVLPLPLPPDSDSDSDAGSGGSSGLRLTAQLLLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          446 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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90US-0523237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D1-dopamine receptor - useful for e.g. drug of e.g. Parkinson's disease or schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Grandy DK, Z
Gingrich JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 552.5; DB 1
Pred. No. 2.8e-45;
9; Mismatches 172
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                                                                                                -HP 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172;
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Best Local S
Matches 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The full-length DNA sequence for the human dopamine D1 receptor was isolated from a lambda EMBL3 SP6-T7 human genomic library. The library was probed by a known 450bp rat D1 clone. Three positive clones with inserts of ca. 14kb were isolated. One of the clones was restriction analysed and sequenced to reveal an open reading frame of 1476 bp encoding a 446 amino acid protein the D1 receptor belongs to the G-protein family; it regulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dopamine D1 receptor; adenylate cyclase stimulation; cAMP-dependent protein kinase activation; psychomotor disorders;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neuron growth and differentiation, modifies D2 receptor-mediated event
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1b; 7pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for studying associated genetic disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleotide base sequence of human dopamine D1 recepts comprises a region susceptible to restriction enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Niznik HB,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human dopamine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                               FTSDLMVGLVVMPPAMLNALYGRWVLARGLCLLWTAFDVMCCSASILNLCLISLDRYLLI 128
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-----CISPGLFDVLTWLGYCNSTMNPIIYPLFMRDFKRALGRFLPCPR-CPRERQA-
                                                    tttgngkpvecsqpessfkmsfkretkvlk---tlsvimgvfvccwlpffilncilpfcg
                                                                                                           TLQVPRTPRPGVESADSRRLATKHSRKALKAKLTLGILLGMFFVTWLPFFVANIVQAVCD
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                                              The murine beta-3 adrenergic receptor gene encodes a polypeptide with 82% homology with the human beta-3 adrenergic receptor. The homology is concentrated in the 7 transmembrane domains. See also AAQ26804-7.
                                                                                                                                                                                                                   Murine adrenergic beta-3-receptor and nucleic acid encoding it for treating diabetes, obesity and hyperlipidaemia, and also for identifying ligands with beta-3 affinity \begin{array}{c} \text{Murine addrenergic beta-3} \\ \text{Murine addrenergic beta-3} \\ \text{Murine addrenergic beta-3} \\ \text{Murine addrenergic beta-3} \\ \text{Murine addrenergic beta-3-receptor and nucleic acid encoding it -100 for the state of the sta
Sequence
                                                                                                                                                                       Claim 13; Page 37;
                                                                                                                                                                                                                                                                                                                                                  WPI; 1992-268668/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-JAN-1991;
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324..344
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290..311
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                                                                                                                       06-JUL-1990;
11-MAR-1993;
19-MAY-1995;
                                                                                                                                                                                                                                                                                       D1 dopamine receptor; activation; adenylyl cyclase activity; coupled; guanine nucleotide binding regulatory protein; drug assessment; agonist; antagonist; efficacy; affinity.
Claim 1; Column 11-16; 24pp; English
                                                                                                                                                                                                                                    Key
Modified-site
                    transformed cells used
                             DNA encoding D1 dopamine receptor protein
                                                 WPI; 1997-178452/16.
N-PSDB; AAT63657.
                                                                               Mahan LC,
                                                                                                                                                               06-JUL-1990;
                                                                                                                                                                                   11-MAR-1997.
                                                                                                                                                                                                       US5610282-A.
                                                                                                                                                                                                                                                                     Rattus rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALGRELPCP---RCPRERQASL--ASP 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GMFFVTWLPFFVANIVQAVC--DCISPGLFDVLTWLGYCNSTMNPIIY---PLFMRDFKR 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lgrfspeesppspsrspspatggtpaapdgvppcgrrparllplrehralr---tlglim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGMASQASETLQVPRTPRP------GVESADSR--RLATKHSRKALKAKLTLGILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aqechsnprc---csfasnmpyallsssvsfylpllvmlfvyarvfvvakrqr-hllrre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----HARPPVPGQCRLLASLPFVLVASGLTFFLPSGAICFTYCRILLAARKQAVQVASLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PALRNTSNEFLVSLFTSDLMVGLVVMPPAMLNALYGRWVLARGLCLLWTAFDVMCCSASI 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pwphrngslalwsdaptldpsaantsglpgvpwaaalagallalatvggnllviiaiart 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGPTANSTPA-WGAGP---PSAPGGSG-----WVAAALCVVIAL-TAAANSLLIALICTQ
                                                                               Mcvittie
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                                                                                                                                                                                                                                                                                                                                receptor
                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                       90US-0548714.
93US-0029917.
95US-0444734.
                                                                                                                                                                90US-0548714.
                                                                                                                                                                                                                                      Location/Qualifiers 45
                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                                                                                                                                            Protein;
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                   for drug screening
                                                                                                                                                                                                                            "N-linked glycosylation site"
                                                                               Monsma
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                                                                                                                                                                                                                                                                                                                                                                                            487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 137;
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                                                                               Sibley
                                                                                DR.
                              for
                              production
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                              of
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AAR15499
ID AAR1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence is the rat D1 dopamine receptor protein which is linked to the activation of adenylyl cyclase activity. The receptor also couples with guanine nucleotide binding regulatory (G) proteins. By constructing cell lines that express the D1 receptor, the affinities and efficacies o agonist and antagonist drugs can be assessed.
                                                                                                                                                                                                                                                                                         catecholamine; G-protein-coupled receptor; neurotransmitter; adenylyl cyclase stimulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR15499 standard;
                Modified-site
                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                       08-MAR-1992 (first entry)
                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                          Rat dopamine D1 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                Modified-site
                                                                                                               Modified-site
                                                                                                                                                                                                                                                            Rattus rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 Match 23.3%; Score 533.5; DB 18; Local Similarity 33.3%; Pred. No. 2.2e-43; nes 134; Conservative 72; Mismatches 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sfyipvaimivtytsiyriaqkqirrisaleraavhakncqttagngnpvecaqsessfk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TFFLPSGAICETYCRILLAARKQAVQVASL-TTGMASQASETLQVPRTPRPGVESADSRR 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAWSLAALASFLPLLLGWHELGHARP--PVPG-----QCRLLASLPFVLVASGL 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  agfwplg-pfcniwvafdimcstasilnlcvisvdrywaisspfqyerkmtpkaafilis 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YGRWYLARGLCLLWTAFDVMCCSASILNLCLISLDRYLLILSPLRYKLRWIPLRALALVL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acflsllilstllgntlvcaavirfrhlrskvtnffvislavsdllvavlvmpwkavaei 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRPGLSLOQVLPLPLPPDSDSDSDSGSGGSSGLRLTAQLLLP 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fgwansslnpily-afnadfgkafstllgcyrlcpttnna-ietvsinnngavvfsshhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGYCNSTMNPIIYPLFMRDFKRALGRFLPCPR-CPRERQASLASPSLR-----TSHSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vawtlsvlisfipvqlswhk---akptwpldgnftsledteddncdtrlsrtyaisssli 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAALCVVIALTAAANSLLIALICTQPALRN-TSNFFLVSLFTSDLMVGLVVMPPAMLNAL
               /note=
268
                                                                                                                                                             /note= "N-glycosylation site -
                                                                                                                                                                                                                            Location/Qualifiers
                                                                            /label= Protein_kinase_A_phosphorylation_site
/note= "putative"
                                                                                                                                                                                             /label=
                            /label= Protein_kinase_A_phosphorylation_site
rnote= "putative"
                                                                                                                                              /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                        "N-glycosylation site -
Protein_kinase_A_phosphorylation_site
                                                                                                                                                OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                           446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 18; Length 487;
                                                                                                                                                                            putative"
                                                                                                                             putative'
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bunzow JR,
Dearry A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cloned gene encoding D1-dopamine receptor - useful for e.g. drug screening, diagnosis of e.g. Parkinson's disease or schizophrenia or in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYDU-)
(UYOR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-MAY-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dependent receptor kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 9; Fig 3A; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-SEP-1990;
14-MAY-1990;
 377
                                                           319
                                                                                                                                                                                202
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                                                                                                                     msfkretkvlk---tlsvimgvfvccwlpffisncmvpfcgseetqpfcidsitfdvfvw 318
                                                                                                                                                                                                         TFFLPSGAICFTYCRILLAARKQAVQVASL-TTGMASQASETLQVPRTPRPGVESADSRR 254
                                                                                                                                                                                                                                        vawtlsvlisfipvqlswhk---akptwpldgnftsledteddncdtrlsrtyaisssli 201
                                                                                                                                                                                                                                                                    GAWSLAALASELPLLLGWHELGHARP--PVPG-----QCRLLASLPFVLVASGL 195
                                                                                                                                                                                                                                                                                                agfwpfg-sfcniwvafdimcstasilnlcvisvdrywaisspfqyerkmtpkaafilis 144
                                                                                                                                                                                                                                                                                                                                                          1991-369177/50
prgsiskdcnlvyliphavgssedlkkeeaggiakpleklsp
                                                                                                                                                  LATKHSRKALKAKLTLGILLGMFFVTWLPFFVANIVQAVCD-----CISPGLFDVLTW 307
                                                                                                                                                                           sfyipvaimivtytsiyriaqkqirrisaleraavhakncqttagngnpvecaqsessfk 261
                                                                                                                                                                                                                                                                                                                  YGRWVLARGLCLLWTAFDVMCCSASILNLCLISLDRYLLILSPLRYKLRWTPLRALALVL 148
                            PRPGLSLQQVLPLPLPPDSDSDSDAGSGGSSGLRLTAQLLLP
                                                                         LGYCNSTMNPIIYPLFMRDFKRALGRFLPCPR-CPRERQASIASPSLR-----
                                                         fgwansslnpiiy-afnadfqkafstllgcyrlcpttnna-ietvsinnngavvfsshhe
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OREGON HEALTH SCI UNIV
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                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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90US-0523237
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                                                                                                                                                                                                                                                                                                                                                                                                                                       23.2%;
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Gingrich JA;
                                                                                                                                                                                                                                                                                                                                                                                                                    72;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 531.5; DB 12; Pred. No. 3.1e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhou OY,
                                                                                                                                                                                                                                                                                                                                                                                                                  158; Indels:
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 418
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         agonist, this activation increasing in the agonist order salbutamol, BRL 28410, BRL 37344 and (I)-isoproterenol; and is recognised by antibodies but not beta 1/2 receptors. The peptide can be used to raise antibodies. Preferred antibodies are directed against the following regions: 1-36, 64-74, 101-108, 133-135, 178-201, 223-291, 314-325, 345-403.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence contains sites necessary (when exposed at a cell surface) for activation of adenylate cyclase in presence of an agonist, this activation increasing in the agonist order salbut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New beta 3 adrenergic receptor polypeptide and encoding nucleic acid - involved in lipolysis, insulin secretion, etc. useful for screening drugs to control these processes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vectors expression the beta 3 receptor gene are plasmids, cosmids or phages, esp. the phage M13mp18-Hubeta3 (CNCM I-883), these are used to transform bacteria or eukaryotic cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beta 3 adrenergic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for screening compounds which can act as specific ligands,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The peptide is implicated in the lipolytic response of adipose tissue, in insulin secretion and in intestinal relaxation. It
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig lbis; 51pp; French.
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      191
                                                                                                                              131
                                                           172 ARPPVPGQCRLLASLPFVLVASGLTFFLPSGAICFTYCRILLAARKQAVQVASLTTGMAS
                                                                                                                                                                                      120
                                                                                                                                                                                                                                                  71
                                                                                                                                                                                                                                                                                                           60
                                                                                                                                                                                                                                                                                                                                                                       11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            1 MVPEPG-PTANSTPAWGAGPPSAPGGSGWVAAALCVVIALTAAANSLLIALICTQPALRN 59
snprc---cafasnmpyvllsssvsfylpllvmlfvyarvfvvatrq----lrllrgelg
                                                                                                                                                                                                                                                                              TSNEFLVSLETSDLMVGLVVMPPAMLNALYGRWVLARGLCLLWTAFDVMCCSASILNLCL 119
                                                                                                                    lavdrylavtnplrygalvtkrcartavvlvwvvsaavsfapimsqwwrvgadaeagrch
                                                                                                                                                          mtnvfvtslaaadlvmgllvvppaatlaltghwplgatgcelwtsvdvlcvtasietlca 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           potentially suitable as drugs for treatment of obesity,
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Pred. No. 3e-43;
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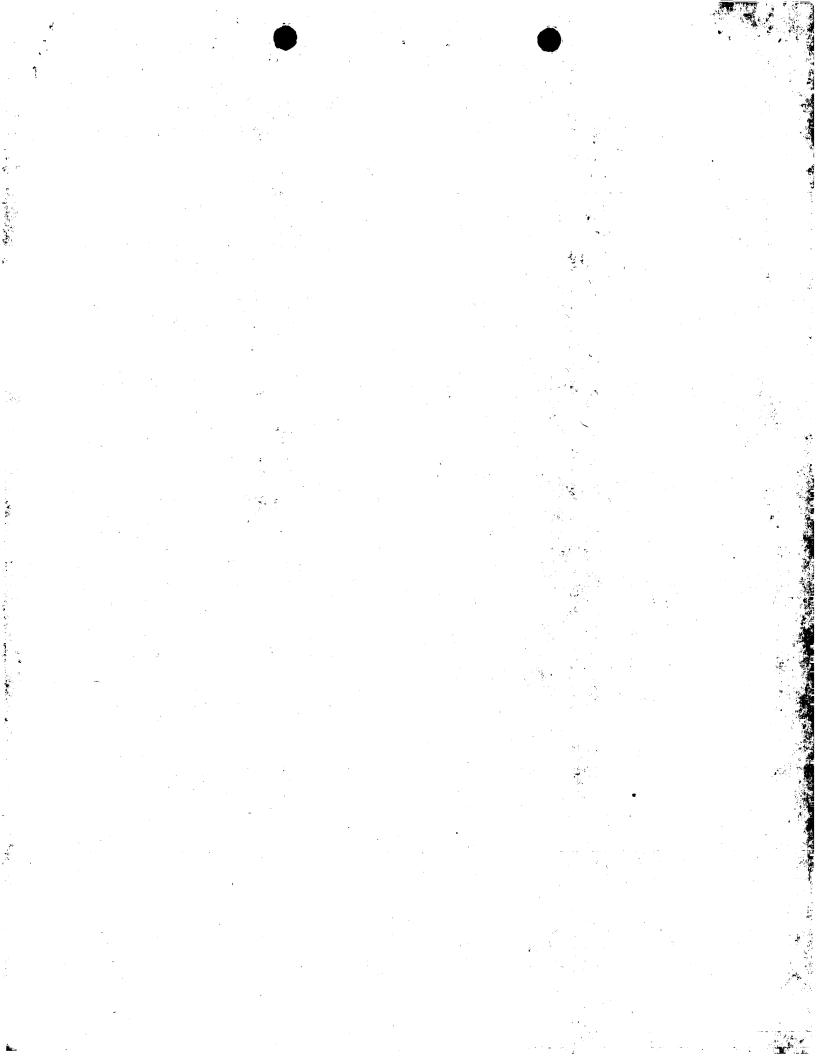
MVPEPG-PTANSTPAWGAGPPSAPGGSGWVAAALCVVIALTAAANSLLIALICTQPALRN 59

lapwpdlptlapntantsglpgvpweaalagallalavlatvggnllvivaiawtprlqt 69

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AAW53847
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                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                   This is the amino acid sequence for the human adrenilin beta-receptor. In the presence of the uncoupling protein (UCP) capable of differentiating or converting into adipocytes. The cells may be used for the analysis of intracellular information transfer and energy metabolism, and development of compositions for the analysis and
                                                                                         metabolism, control of
                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                           Preparing cultured cells capable of converting into adypocytes transferring cells with human adrenalin beta receptor and
                                                                                                                                                                                                                                             N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human adrenaline beta-receptor
                                                         Sequence
                                                                                prevention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human adrenilin beta-receptor;
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                                                                                                                                                                         Example 1; Fig 6; 8pp; Japanese
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                                                                                            these systems.
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/product= "human adrenaline beta-receptor
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 Score 531; DB 19;
Pred. No. 3.1e-43;
2; Mismatches 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uncoupling
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                                                                                                            70 mtnvfvtslaaadlvmgllvvppaatlaltghwplgatgcelwtsvdvlcvtasietlca 129
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Search completed: March 15, 2002, 14:11:21 Job time: 116 sec



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DADR_DIDMA
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028927 ovis aries
P26255 rattus norv
09xt57 capra hircu
077680 macaca mula
P35406 carassius a
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## ALIGNMENTS

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requires a license an email to license en email en	his his he he se odi		[2] SEQUENCE OF 215-280 FROM N.A. SISSUE-Striatum; TISSUE-Striatum; MEDLINE-95385798; PubMed=7656980; Ullmer C., Schmuck K., Kalkman H.O., Lubbert H.; "Expression of serotonin receptor mRNAs in blood vessels."; FIBS Lett. 370:215-221(1995)i- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  TISSUE-Striatum;  MEDLINE-96102917; PubMed-8522988;  KOHEN R., Metcalf M.A., Khan N., Druck T., Huebner K., Lachowicz J.E.,  Sibley D.R., Roth B., Hamblin M.W.;  "Cloning, Characterization, and chromosomal localization of a human 5-HTG serotonin receptor";  J., Neurochem. 66:47-56(1996).	ordata; Craniata; imates; Catarrhin	HUMAN  STANDARD; PRT; 440 AA.  P50406; Q13640; 01-OCT-1996 (Rel. 34, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) 5-HYDROXYTRYPTAMINE 6 RECEPTOR (5-HT-6) (SEROTONIN RECEPTOR).

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RESULT 2
5H6_MOUSE
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Best Local
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Q9R1C8;
20-AUG-2001
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                20-AUG-2001 (Rel. 40,
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5-HYDROXYTRYPTAMINE 6
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99.8%;
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                                           Last sequence update)
Last annotation update)
RECEPTOR (5-HT-6) (SEROTONIN RECEPTOR).
                                                                               Created)
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1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL)
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Pred. No. 5
      Craniata; Vertebrata;
Sciurognathi; Muridae.
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7 (POTENTIAL).
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       Muridae; Murinae;
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Matches 387; Conserv
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Multigene
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Mutagenesis studies of the mouse 5-HT6 serotonin receptor.";

Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-HYDROXYTEXPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTION.

A NEUROTRANSMITTER, A HORMONE, AND A MITGGEN. THE ACTIVITY OF THE RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATES ADENVLATE CYCLASE. IT HAS A HIGH AFFINITY FOR TRICYCLIC PSYCHOTROPIC DRUGS

(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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STRAIN=129/SVJ; TISSUE-Brain;
STRAIN=129/SVJ; TISSUE-Brain;
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
VPRTPRPGVESADSRRLATKHSRKALKAKLTLGILLGMFFVTWLPFFVANIVQAVCDCIS
                                                                                                                                  SLDRYLLILSPLRYKLRMTPLRALALVLGAMSLAALASFLPLLLGWHELGHARPPVPGQC 180
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                                                      PF00001;
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87.6%;
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5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELULAR (POTENTIAL).

7 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).
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CYTOPLASMIC (P
BY SIMILARITY.
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Pred. No. 2.7e-118;
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EXTRACELLULAR (POTENTIAL)

5 (POTENTIAL)
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RESULT
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SEQUENCE FROM N.A.
MEDLINE=93277562; PubMed=8389146;
MEDLINE=9327760rt E., Arrang J.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-Striatum;
MEDLINE-93196608; PubMed-7680751;
MONSMA F.J. Jr., Shen Y., Ward R.P., Hamblin
"Cloning and expression of a novel serotonin
affinity for tricyclic psychotropic drugs.";
MO1. Pharmacol. 43:320-327(1993).
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P31388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1993 (Rel. 26, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
5-HYDROXYTRYPTAMINE 6 RECEPTOR (5-HT-6) (SERO
 EMBL;
EMBL;
EMBL;
GCRDb;
                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Leurs R., Schwartz J.-C.
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                                                                                                                                                                                                                                                                                                                                                                        Martial R.;
                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-WISTAR;
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Blochem. Blophys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTR6
                                                                                                                                                                                                                                                                                                                                                                                                                                  "A novel rat serotonin (5-HT6) receptor: molecular clocalization and stimulation of cAMP accumulation."; Blochem. Blophys. Res. Commun. 193:268-276(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ST-B17).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     419
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                                                                                                                                                                                               CYCLASE. IT HAS A HIGH AFFINITY FOR TRICYCLIC PSYCHOTROPIC DRUG SUBCELULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: LOCALIZED EXCLUSIVELY IN THE CENTRAL NERVOL SYSTEM, PREDOMINARTLY IN THE CORPUS STRIATUM BUT ALSO IN VARIOU LIMBIC AND CORTICAL REGIONS.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                            FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTION AS A NEUROTEANSMITTER, A HORMONE, AND A MITGGEN. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATES ADENYLATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ω
; L03202; AAA40618.1;
; S62043; AAB26908.1;
; L19656; AAA40611.1;
b; GCR_0723; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NFFVTDSVEPEIRQHPLGSPMN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGLFDVLTWLGYCNSTMNPIIYPLFMRDFKRALGREVPCVHCPPEHRASPASPSMWTSHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VPRTPRPGMESADSRRLTTKHSRKALKASLTLGILLSMFFVTWLPFFVASIAQAVCDCIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGLFDVLTWLGYCNSTMNPIIYPLFMRDFKRALGRFLPCPRCPRERQASLASPSLRTSHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                           to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tardivel-Lacombe J., Diaz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         м.
Ж.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor with high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cloning,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sibley D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
; Murinae; Rat
                                                                                                                                                                                                                                  VARIOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus
                                                                                                                                                                                                                                                                               DRUGS
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RESULT 4
B1AR\_MOUSE
ID BLAR\_MOUSE
AC P34971;
DT 01-FEB-1994
DT 01-FCB-1994
DT 01-FCB-1994
DT 01-NOV-1995
DE BETA-1 ADRE

STANDARD;

PRT;

466

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01-FEB-1994 01-FEB-1994 01-NOV-1995

3-1994 (Rel. 3-1994 (Rel. 7-1995 (Rel. L ADRENERGIC

. 28, Created)
. 28, Last sequence upo
. 32, Last annotation of RECEPTOR.

update)

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Best Local :
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Multigene
DOMAIN
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DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00237; GPCKRHODOPSN.
PRINTS; PR01102; 5HT6RECEPTR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                           CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCRDb; GCR_0719;
301
                301
                                  241
                                                   241
                                                                   181
                                                                                     181
                                                                                                      121
                                                                                                                       121
                                                                                                                                        61
                                                                                                                                                        61
                                                                                                                                                                                  1 MYPEPGPTANSTPAWGAGPPSAPGGSGWVAAALCVVIALTAAANSLLIALICTQPALRNT
         LFDVLTWLGYCNSTMNPIIYPLFMRDFKRALGRFLPCPRCPRERQASLASP
                                RLLASLPFVLVASGVTFFLPSGAICFTYCRILLAARKQAVQVASLTTGTAGQALETLQVP
                                                                            RLLASLPFVLVASGLTFFLPSGAICFTYCRILLAARKQAVQVASLTTGMASQASETLQVP
                                                                                                              SLDRYLLILSPLRYKLRMTPLRALALVLGAWSLAALASFLPLLLGWHELGHARPPVPGQC
                                                                                                                                        SNFFLVSLFTSDLMVGLVVMPPAMLNALYGRWVLARGLCLLWTAFDVMCCSASILNLCLI
                                                                                                                                                                           MVPEPGPVNSSTPAWGPGPPPAPGGSGWVAAALCVVIVLTAAANSLLIVLICTQPALRNT
LFDVLTWLGYCNSTMNPIIYPLFMRDFKRALGRFLPCVHCPPEHRPALPPP
                                                                                                      SLDRYLLILSPLRYKLRMTAPRALALILGAWSLAALASFLPLLLGWHELGKARTPAPGQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            family.
                                                                                                                                                                                                                                                       436
                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor;
                                                                                                                                                                                                                                                                                                          46922 MW;
                                                                                                                                                                                                                    73.2%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                   5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
                                                                                                                                                                                                             6;
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (POTENTIAL).
CYTOPLASMIC (P.
2 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane;
                                                                                                                                                                                                                                                                                                                                  7 (POTENTIAL).
CYTOPLASMIC (POTENT)
N-LINKED (GLCNAC...
                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL)
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                     Score 1678;
Pred. No. 9
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                                                                                                                                                                                                                                                                       DLSQRCQTRPQLQQVLALPLPPNSDSDSASGGTSGLQLTAQ
LLLPGEATRDPPPPTRATTVVNFFVTDSVEPEIRPHPLSSP
                                                                                                                                                                                                                                                                                        L -> V (IN REF. 1).

PCVHCPPEHRPALPPPPCGPLTAVPDQASACSRCCLCLCRQ
PCVHCPPEHRPALPSPPCCLEEEPPGTPHHPPGPPLWST
SLSQTLWSLRYGRIHSVPP -> HASTVPRSTGQPCLPLHV
                                                                                                                                                                                                                                                                                                                                                                                      4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                           BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                       6BC00F6A3CBA5FB4 CRC64;
                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                     DB 1;
).1e-99;
                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein;
                                                                                                                                                                                                                                                                                                                                    .) (POTENITAL).
                                                                                                                                                                                                                             Length 436;
351
                 351
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                                                                                                                                                                                                            Gaps
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Best Local S
Matches 158
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MOD_RES
SEQUENCE
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Jasper J.R., Link R.E., Chruscinski A.J., Kobilka B.K., Bernstein D
Jasper J.R., Link R.E., Chruscinski A.J., Kobilka B.K., Bernstein D
"Primary structure of the mouse beta 1-adrenergic receptor gene.";

Biochim. Biophys. Acta 1178:307-309(1993).

-i- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
INDUCED ACTIVATION OF ADENULATE CYCLASE THROUGH THE ACTION OF G
PROTEINS. THIS RECEPTOR BINDS EPIMEPHRINE AND NOREPINEPHRINE WI
APPROXIMATIVELY EQUAL AFFIRITY.

-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-i- PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY
PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE.

-I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                             G-protein
Multigene
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR00561; ADRENRGCBIAR.
PRINTS; PR01103; ADRENRGCFIAR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Phosphorylation; Lipoprotein; Palmitate.
                                                                                                                                                                  LIPID
                                                                                                                                                                               DISULFID
                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L10084; AAA02929.1; PIR; S36794; S36794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
                                                                                                                                                     MOD_RES
                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                               TRANSMEM
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Pfam; PF00001; 7tm_1; 1.
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European Bioinformatics Institute. There a
by non-profit institutions as long as i
PTANSTPAWGAGPPSAPGGSGWVAA----ALCVVIALTAAANSLLIALICTQPALRNTSNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            b; GCR_0578; -.
MGI:87937; Adrb1.
                                          al Similarity
158; Conser
                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDEP.
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83
120
120
131
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50479
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Rodentia;
                                                    25.8%;
35.9%;
                                                                                                            WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .'
                                          63;
                                                                                                                                                                                                                 1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).

2 (POTENTIAL).

3 (POTENTIAL).

3 (POTENTIAL).

4 (POTENTIAL).

4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).
                                     Score 591.5; Db 1,
Pred. No. 1.6e-30;
""smatches 154;
                                                                                                                        PHOSPHORYLATION PHOSPHORYLATION
                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (
                                                                                                                                                               BY SIMILARITY.
PALMITATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                          IOSPHORYLATION (BY CAPK)
IOSPHORYLATION (BY CAPK)
IOSPHORYLATION (BY CAPK)
753CD44C42BC9211 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no rest
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                                         Indels
                                                                  Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         restrictions
                                                                                                                     (POTENTIAL)
                                                                                                                                                 (POTENTIAL)
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RESULT 5
Blar_Canfa
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01-NOV-1997
15-JUL-1998
EMBL; U73207; AAB93648.1; -. HSSP; P07700; IDEP.
                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                               the
                                                                                                                                                                                     This
                                                                                                                                                                                                                                                                                                                                               J. Recept. Signal Transduct. Res. 17:599-607(1997).

- FUNCTION: BETA-ABRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
INDUCED ACTIVATION OF ADENVLATE CYCLASE THROUGH THE ACTION OF PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE W
                                                                                                                                                                between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Huang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=97364078; PubMed=9220370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
Mammalia; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BETA-1 ADRENERGIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P79148;
                                                                                                                                                                                                                                                                                                                                                                                                                                    receptors."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fong T.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Canis familiaris (Dog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Molecular cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            437
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                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS

PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE
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35, Last sequence update)
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PRINTS; PR00561; ADRENNGCBIAR.
PRINTS; PR01103; ADRENNGCBIAR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Phosphorylation; Lipoprotein; Palmitat
BIAR_RAT STANDARD;
P18090;
01-NOV-1990 (Rel. 16, Created)
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CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).

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EXTRACELLULAR (POTENTIAL).

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CYTOPLASMIC (POTENTIAL).

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EXTRACELLULAR (POTENTIAL).

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Neve K.A., Tear ...
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"molecular gene.";
receptor gene.";
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PRINTS; PRO01317; GPCRRIODOPSN.
PRINTS; PRO01103; ADRENARGCBLAR.
PRINTS; PRO01103; ADRENARGICR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
G-PROTEIN_RECEP_F1_2; 1.
G-PROTEIN_RECEP_F1_2; 1.
G-PROTEIN_RECEP_F1_2; 1.
G-PROTEIN_RECEP_F1_2; 1.
Multigene family; Phosphorylation; Lipoprotein; Palmitat Multigene family; Phosphorylation; Lipoprotein; Palmitat DOMAIN

1 59
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
 DISULFID
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MEDLINE-90330633; Pubmed-1695899;

Machida C.A., Bunzow J.R., Searles R.P., v.

Machida C.A., Teal P., Nipper V., Civelli O.;

Neve K.A., Teal P., Nipper V., Civelli O.;
                                                                                                                                                                                                                                                                                                                                                                                                       GCRDb; GCR_0126; -.
GCRDb; GCR_0127; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A36618; A36618.
PIR; S12591; S12591.
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Mammalia; Eutheria;
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 Chordata;
Rodentia;
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                                                                                              3 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).
                                                                                                                                                                                           1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).
               CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (PROBABLE).
BY SIMILARITY.
                                                                 EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
                                                                (POTENTIAL)
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                                  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
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32, Last
                                                                                                                                                                                                                                                                                expression of the rat beta 1-adrenergic
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annotation update)
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Matches 156
                                                                                                                                                                                                                                      20-AUG-2001 (Rel. 4
20-AUG-2001 (Rel. 4
20-AUG-2001 (Rel. 4
BETA-1 ADRENERGIC F
                                    "Felis domesticus beta adrenergic receptor subtype 1.";
Submitted (OCT-1999) to the EMEL/GenBank/DDBJ databases.
-i- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF GPROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND MOREPINEPHRINE WIS APPROXIMATIVELY EQUAL AFFINITY (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-i- PTM: HOMOLOGOUS DESENSITIZATION OF THE BECTAMAN-1-
-i- PTM: HOMOLOGOUS DESENSITIZATION OF THE BECTAMAN-1-
                                                                                                                                                                                                                                                  20-AUG-2001
20-AUG-2001
20-AUG-2001
                                                                                                                                                                           Eukaryota; Metazoa; Chordata; (
Mammalia; Eutheria; Carnivora; 
MCBI_TaxID=9685;
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Q9TST6;
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       SIMILARITY).
SIMILARITY: BELONGS
                               PTM: HOMOLOGOUS DESENSITIZATION OF PHOSPHORYLATION BY BETA-ADRENERGIC
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Chordata; Craniata; Vertebrata;
Chordata; Fissipedia; Felidae;
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Pred. No. 3.2e
63; Mismatches
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PRINTS; PRO10237; GPCRENORGCBIAR.
PRINTS; PRO1103; ADRENARGICE.
PROSITE; PSO0237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PSO0237; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PSO0237; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PSO0262; G_PROTEIN_RECEP_F1_2; 1.
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DAGSGGSSGLRLTAQLLLPGEATQDPPLPTRAAAAVNFFNID-PAEP
                                                                                           LGMFFYTWLPFFYANIYQAV-CDCISPGLFDVLTWLGYCNSTMNPIIY---PLFMRDFKR
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                             AFQRLL-
                                                   ALGRELPCPRCPRERQASLASPSLRTSH--SGPRPGLS--LQQVLPLPLP---PDSDSDS
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                                                                             MGVFTLCWLPFFLANVVKAFHRDLVPDRLFVFFNWLGYANSAFNPIIYCRSP----DFRK
                                                                                                                                ARPPSPA~PAPGSPRPAATAAAAAAAAPLANGRISKRRPSRLVALREQKALK---
                                                                                                                                                             ASQASETLQVPRTPRPGVESADS ---
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                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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34.78;
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4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTY...

6 (POTENTY...
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
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Pred.
                          RGGHAAAGDRPRASGCLPGTRPPPSPGAASDEDDDD
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PALMITATE (BY SIMILARITY).
; 2FC97EDE4CFB7C3F CRC64;
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CYTOPLASMIC (POTENT)
N-LINKED (GLCNAC...
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No. 3.1e-29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                           Length 474;
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В

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RESULT

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Blar_MACMU
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MEDLINE=95078456; PubMed=7987008;

MEDLINE=95078456; PubMed=7987008;

Searles R.P., Nipper V.J., Machida C.A.;

Searles R.P., Nipper V.J., Machida C.A.;

The rhesus macaque beta 1-adrenergic receptor gene: structure of 1 gene and comparison of the flanking sequences with the rat beta 1-adrenergic receptor gene.";

DNA Seq. 4:231-241(1994).

-I- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-INDUCED ACTIVATION OF ADENULATE CYCLASE THROUGH THE ACTION OF PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1996
01-FEB-1996
15-JUL-1998
         DISULFID MOD_RES
                                                                             TRANSMEM
DOMAIN
                                                                                                                                               DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR00561; ADRENRGCBIAR.
PRINTS; PR01103; ADRENRGGICR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                          G-protein
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HSSP; P07700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Macaca mulatta (Rhesus macaque)
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                                                      CARBOHYD
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                                                                                                                          DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPROXIMATIVELY EQUAL AFFINITY.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY
PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a sen the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pro; IPR000276; GPCR_Rhodpsn
PF00001; 7tm_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                     family;
                                                                                                                                                                                                                                                                                                                                                                                                                                          coupled receptor;
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33, Last sequence update)
36, Last annotation update)
RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                        Phosphorylation;
         license agreement
EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).

4 (POTENTIAL).

4 (POTENTIAL).

5 (POTENTIAL).

5 (POTENTIAL).

6 (POTENTIAL).

6 (POTENTIAL).

7 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

OTTOPLASMIC (POTENTIAL).

7 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

OTTOPLASMIC (POTENTIAL).

PHOSPHORYLATION (BY CAPK) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane; Glycoprotein; Lipoprotein; Palmitat exTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                            1 (POTENTIAL).
CYTOPLASMIC (P.
2 (POTENTIAL).
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Best Local
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Mammalia; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD_RES
      SEQUENCE FROM N.A. MEDLINE=98318327; Publ Cao H., Bidwell C.A.,
                                                                                                                                                                                                                                                      Q28998; O46575;
15-JUL-1998 (Rel. 36, Created)
15-DEC-1998 (Rel. 37, Last seq
15-JUL-1999 (Rel. 38, Last ann
                                                                                                                "Nucleotide sequence of the coding adrenergic receptor gene."; J. Anim. Sci. 76:1720-1721(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                  Blar_PIG
                                                                        McNeel R.L., Mersmann
                                                                                  TISSUE=Heart;
                                                                                             SEQUENCE OF 101-468
                                                                                                                                                                                         NCBI_TaxID=9823;
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149; Conser
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Eutheria;
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                                                                                                                                                PubMed=9655595;
.A., Williams S.K.,
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395
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DESENSITIZATION OF
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Cetartiodactyla; Suina;
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annotation update)
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Pred. No. 9.1e
62; Mismatches
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ina; Suidae;
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1es 166;
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MEDIATED BY
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Best Local Similarity
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the European Bioinformatics Institute. The
use by non-profit institutions as long a
modified and this statement is not removed.
entities requires a license agreement (See |
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                      MVPEPGPTANSTPA----
---TGMASQASETLQVPRTPRPGVESA---
                                                                     GAEARRCYNDPKCCDFVTNRAYAIASSVVSFYVPLCIMAFVYLRVFREAQKQVKKIDSCE
                                                                                                                   LGHARPPV--PGQCRLLASLPFVLVASGLTFFLPSGAICFTYCRILLAARKQAVQVASLT
                                                                                                                                                                 TASIETLCVIALDRYLAITSPFRYQSLLT-RAARALVCTVWAISALVSFLPILMHWWRDK
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                                                                                                                                                                                                                                                                  IAKTPRLQTLTNLFIMSLASADLVMGLLVVPFGATIVVWGRWEYGSFFCELWTSVDVLCV
                                                                                                                                                                                                                                                                                                                                                                   LVPASPPASLLTPASEGSVQLSQQWTAG------MGLLMALIVLLIVAGNVLVIVA
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L -> V (IN REF. 2).
CWL -> WWV (IN REF. 2).
R -> A (IN REF. 2).
T -> S (IN REF. 2).
AS -> SF (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 559; DB 1;
Pred. No. 1.7e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (POTENTIAL).
BY SIMILARITY.
PALMITATE (BY SIMILARITY).
A -> AR (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     There are no rest
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TEF. 2).

TEF. 2).

TEF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 468;
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                       272
                                                                                                                                                                 201
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B3AR_CANFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Вb
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                           TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Thompson G.M., Kelly L.J., Candelore M.R.;

Thompson G.M., Kelly L.J., Candelore M.R.;

Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF A

INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF A

TOTAL PROPERTY OF THE PROPERTY 
                                                                   TRANSMEM
DOMAIN
                                                                                                                                                                              PROSITE; PROSITE;
                                                                                                                                                                                                                     PRINTS; PR00237; GPCRRHODDPSN.
PRINTS; PR00563; ADRENGGCB3AR.
PRINTS; PR01103; ADRENERGICR.
                                                                                                                                                           G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entitles requires a license agreement (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADRES ON CONTROL (Dog).
Canis familiaris (Dog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota, Putheria: Carnivora; Fissipedia; Canidae;
      TRANSMEM
                                                                                                                               Multigene
                                                                                                                                                                                                                                                                                           Pfam; PF00001; 7tm_1; 1
                                                                                                                                                                                                                                                                                                                                       EMBL; AF200597; AA HSSP; P07700; 1DEP
                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U92468; AAB51068
                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel.
15-JUL-1999 (Rel.
BETA-3 ADRENERGIC
                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between
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01-NOV-1997 (Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          canine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archimbault P., Strosberg A.D.; "Genomic cloning and species-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=99095920; PubMed=9881593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B3AR_CANFA
                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eur. J. Pharmacol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lenzen G., Pietri-Rouxel F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9615;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: INTEGRAL SIMILARITY: BELONGS TO FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAP-----PAPLLEPWAGYNGGAARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSGGSSGLRLTAQLLLP----GEATQD 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KAFQRLLCCAR-----RVARGSCAAAGDGPRASGCLAVARPPPSPGAASDDDDDEEDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RALGRFLPCPRCPRERQASLASPSLRTSHSGPRPGLSLQQVLPLPLP----PDSDSDSDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMGVETLCWLPEFLANVVKAFHRDLVPDRLEVFFNWLGYANSAFNPIIYCRSP----DFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLGMFFVTWLPFFVANIVQAV-CDCISPGLFDVLTWLGYCNSTMNPIIY---PLFMRDFK
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                                                                                                                                                                              PS00237;
PS50262;
                                                                                                                                                         coupled
                                                                                                                                    tamily;
                                                                                                                                                                                                                                                                                                             IPR000276; GPCR_Rhodpsn
    37
64
73
92
112
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                                                                                                                                                                                                                                                                                                                                                            AAF08307.1;
                                                                                                                               G_PROTEIN_RECEP_F1_1; 1.
g_PROTEIN_RECEP_F1_2; 1.
receptor: Transmembrane; Glycoprotein;
Phosphorylation; Lipoprotein; Palmitat
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O FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).
                                                                                                      EXTRACELLULAR (POTENTIAL).
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                                                                                                                               Palmitate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        328
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RESULT 11
BLAR_BOVIN STAN
ID BLAR_BOVIN STAN
AC Q9TT96; Q9TUB4;
DT 20-AUG-2001 (Rel. 4
DT 20-AUG-2001 (Rel. 4
DT 20-AUG-2001 (Rel. 4
DT 20-AUG-2001 (Rel. 4
DE BETA-1 ADRENERGIC R
GN ADRBI.
OS BOS taurus (Bovine)
OC Eukaryota; Metazoa;
OC Mammalia; Eutheria;
OC Mammalia; Eutheria;
OC Mammalia; Bovinae; B
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Ha S.H., Balk M.G.,
RA Ha S.H., Balk M.G.,
RA Ha S.H., Balk M.G.,
RA SEQUENCE OF 90-367
RN [2]
RP SEQUENCE OF 90-367
RR SEQUENCE OF 90-367
RR SEQUENCE OF 90-367
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Best Local Similarity
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DOMAIN
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CARBOHYD
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CONFLICT
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DOMAIN
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DOMAIN
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                                                                                                                                                                                                                     C-RCRREEHRAAASP-----PGDPSAAPAALTSPAES-SRCQALDGASWGI
                                                                                                                                                                                                                                                                                                                                                                                                      CPRCPRERQASLASPSLRTSHSGPRPGLSLQQVLPLPLPDSDSDSDAGSGGSSGL
                                                                                                                                                                                                                                                                    PFFVANIVQAVCD---CISPGLFDVLTWLGYCNSTMNPIIY---PLFMRDFKRALGRFLP
                                                                                                                                                                                                                                                                                                                                                                                      DRYLLILSPLRYKLRMTPLRALALVLGAWSLAALASFLPLLLGWHELG------
                                                                                                                                                                                                                                                                                             SPPAASRSRSPGPARRCASPAAVPSDRLRPARLLPLREHRALR---
                                                                                                                                                                                                                                                                                                       ETLQVPRTPRPG------VESADSR--RLATKHSRKALKAKLTLGILLGMFFVTWL
                                                                                                                                                                                                                                                                                                                               HC---CAFASNIPYALLSSSVSFYLPLLVMLFVYARVFLVATRQ-LRLLRRELGRFPPAE
                                                                                                                                                                                                                                                                                                                                                                    DRYLAVTNPLRYGALVTKRRARAAVVLVWVVSAAVSFAPIMSKWWRVGADAEAQRCHSNP
                                                                                                                                                                                                                                                                                                                                                                                                                                             PTPTPDAANT - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148;
                                                                                         Eutheria;
                                                                                                            (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           405
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348
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361
            90-367
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                                                                                                                                                                         STANDARD;
 TISSUE-Adipocyte;
                                                                                                                              40, Created)
40, Last sequence update)
40, Last annotation updat
RECEPTOR.
                                                                                  Bos.
            FROM N.A
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178
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225
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189
361
                                              Choi Y.J.;
                                                                                          Cetartiodactyla;
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                                                                                                   Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

BY SIMILARITY.

PALMITATE (BY SIMILARITY).

Q -> P (IN REF. 2).

A -> V (IN REF. 2).

MW; 1A4E3EBBBC9D047F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).

4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).
                            receptor from Kor
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
                                                                                                   Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     558.5; DB 1
No. 1.6e-28;
                                     from Korean cattle.";
                                                                                          Ruminantia;
                                                                                                                                                                         467
                                                                                                                                     update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154;
                                                                                        Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                            TLGLIVGTFTLCWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                405;
                                                                                          Bovoidea
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                                                                                                                                                                                                                                                                                                                                                                    193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
Ş
                  B
                                   Q
                                                      Db
                                                                       Qy
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R PRINTS; PRO0237; GECRHODOPSN.

R PRINTS; PR00237; GECRHODOPSN.

R PRINTS; PR00131; ADRENERGICAR.

R PRINTS; PR00131; ADRENERGICE_F1_1; 1.

R PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.

R PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.

W G_POTOTEIN coupled receptor; Transmembrane; Glycoprotein; Wiltigene family; Phosphorylation; Lipoprotein; Palmitate.

Multigene family; Phosphorylation; Lipoprotein; Palmitate.

T DOMAIN 1 59 EXTRACELULIAR (POTENTIAL).

T TRANSMEM 60 83 1 (POTENTIAL).

T TRANSMEM 97 121 2 (POTENTIAL).

T TRANSMEM 97 121 2 (POTENTIAL).

T TRANSMEM 133 153 3 (POTENTIAL).

T TRANSMEM 133 153 3 (POTENTIAL).

T TRANSMEM 133 153 3 (POTENTIAL).
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the European Bioinformatics Institute
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                          QTLTNLFINSLASADLVMGLLVVPFGATIVVMGRWEYGSFFCELWTSVDVLCVTASIETL
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CYTOPLASMIC (POTENTIAL).

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G -> D (IN REF. 1).

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                                                                                                                                                                                                                                                                     Moore J.D., Mason D.A., Green S.A., Hsu J., Liggett S.B.; "Racial differences in the frequencies of cardiac beta(1)-adrenergic receptor polymorphisms: analysis of c145A>G and c1165G>C.";
                                                                                                                                                     receptor
                                                                                                                                                                                                      MEDLINE=20507547; PubMed=11052857;
                                                                                                                                                                                                                                                                                                                                                                                Mason D.A., Moore J.D., Green S.A., Li
"A gain-of-function polymorphism in a
human betal-adrenergic receptor.",
J. Biol. Chem. 274:12670-12674(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99230291;
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                                                                                                                                                                                                                            VARIANT GLY-49
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Proc. Natl. Acad. Sci. U.S.A. 84:7920-7924(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rISSUE=Placenta;
MEDLINE=8068509; PubMed=2825170;
MEDLINE=8068509; PubMed=2825170;
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novel polymorphism in the gene coding for the beta(1)-adrenergic eptor associated with survival in patients with heart failure.";

Heart J. 21:1853-1858(2000).

FUNCTION. BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH APPROXIMATIVELY EQUAL AFFINITY.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY ITS PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE.
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the beta(1)-adrenergic
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PRINTS; PR00237; GPRENGCBLAR.

PRINTS; PR00561; ADRENGCBLAR.

PRINTS; PR01103; ADRENGGICR.

PROSTITE; PS01237; G_PROTEIN_RECEP_F1_1; 1.

PROSTITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.

PROSTITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.

PROSTITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.

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PIR; A39911; A39911.
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                       PGQCRLLASLPFVLVASGLTFFLPSGAICFTYCRILLAARKQAVQVAS----LTTGMASQ 232
                                                  ALDRYLAITSPFRYQSLLTRARARGLVCTVWAISALVSFLPILMHWWRAESDEARRCYND
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation updat
BETA-3 ADRENERGIC RECEPTOR.
                                                                                                                                  Casteilla L., Muzzin P., Revelli J.-P., Ricquier D., Giacobino Expression of beta 1- and beta 3-adrenergic-receptor messages adenylate cyclase beta-adrenergic response in bovine perirenal tissue during its transformation from brown into white fat."; Blochem. J. 297.93-97.1994).
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J. Anim. Sci. 78:1397-1398(2000).
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Strosberg A.D., Manning B.S.J.; "Molecular cloning and pharmacological beta 3-adrenergic receptor"; Eur. J. Biochem. 230:350-358(1995).
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Pietri-Rouxel F., Lenzen G., Kapoor
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Bovidae; Bovinae; B
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MEDLINE-94107292; PubMed-7904157;
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                                                    SUBCELLULAR LOCATION:
SIMILARITY: BELONGS T
             SWISS\text{-PROT} entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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 -CPRCPRERQASLASPSLRTSHSGPRPGLSLQQVLPLPLPPDSDSDSDAGS
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42903
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BY SIMILARITY.
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5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 554; DB 1;
Pred. No. 3.1e-28;
1; Mismatches 156
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PG -> HE (IN REF. 3).
A -> T (IN REF. 4).
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CYTOPLASMIC (
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CYTOPLASMIC (
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361

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J. Anim. Sci. 78:1397-1398(2000).

-i- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
PROTEINS. BETA-3 IS INVOLVED IN THE REGULATION OF LIPOLYSIS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --, --, metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
         DISULFID
                                CARBOHYD
                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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20-AUG-2001 (Rel.
BETA-3 ADRENERGIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Forrest R.H., Hickford J.G.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20292453; PubMed=10834601;
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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. 40, Last sequence upo
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EXTRACELULAR (POTENTIAL).

3 (POTENTIAL).

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EXTRACELLULAR (POTENTIAL).

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Best Local Similarity 34.3
Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            P25962; 090Z98;
01-MAY-1992 (Rel. 22, Created)
01-FEB-1994 (Rel. 28, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
BETA-3 ADRENERGIC RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIPID
SEQUENCE
                                        SEQUENCE FROM N.A. (ISOFORM B). STRAIN=C57BL/6; TISSUE=Brown adipomedLINE=99396494; PubMed=10455305
                                                                                             "The promoter and intron/exon structu 3-adrenergic-receptor genes."; Eur. J. Biochem. 213:1117-1124(1993).
                                                                                                                                                                                                                                           MEDLINE=92037534; Put
Nahmias C., Blin N.,
Emorine L.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOUSE
                "Alternative
                                                                                                                                                                REVISIONS, SEQUENCE FROM N.A. MEDLINE=93279311; PubMed=8389293;
                                                                                                                                                                                                     "Molecular characterization of the mouse relationship with the atypical receptor c EMBO J. 10:3721-3727(1991).
                                                                                                                                     Strosberg A.D.,
                                                                                                                                                 van Spronsen A.,
                                                                                                                                                                                                                                                                                        STRAIN-SWISS
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                    ADRB3 OR ADRB3R OR B3BAR.
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405 AA;
                            Papaioannou M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                     Emorine L.J.;
                                                                                                                                                  Nahmias C., Krief
                                                                                                                                                                                                                                                         PubMed=1718744;
N., Elalouf J.M.,
                                                                                                                                                                                                                                                                                                                                        Chordata;
Rodentia;
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Pred. No. 3.3e-28;
6; Mismatches 165;
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R.J.;
the beta3-adrenoceptor
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which are differentially expressed in mouse tissues.", Br. J. Pharmacol. 127:1525-1531(1999).

SEQUENCE OF 378-400 FROM N.A.

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PIR; S18548; S18548.
PIR; S32804; S32804.
HSSP; P07700; 1DEP.
GCRDb; GCR_0253; -.
                                                                                                                                                                                                                                                                                           Interpro; IPR000276; GPCR_Rhody pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRHODOPSN.
PRINTS; PR00563; ADRENRGCB3AR.
PRINTS; PR01103; ADRENERGICR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restriuse by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Granneman J.G., Lahners K.N., Rao D.D.;

"Rodent and human beta 3-adrenergic receptor genes contain 
"thin the protein-coding block.";
    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement
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ALTERNATIVE PRODUCTS: 2 ISOFORMS; ISOFORM A (SHOWN HERE)
ISOFORM B; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: WHITE AND BROWN ADIFOSE TISSUES, AND
TRACT. ISOFORM B HIGHEST IN BRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . Pharmacol. 42:964-970(1992).
FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
PROTEINS. BETA-3 IS INVOLVED IN THE REGULATION OF LIPOLYSIS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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    MW;
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
BY SIMILARITY
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ISOFORM B).
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## ALIGNMENTS

N.Alternate names: 5-hydroxytryptamine receptor 6 (5 C; Species: Homo sapiens (man) (C; Date: 02-Sep-1997 \*sequence\_revision 05-Sep-1997 # C; Accession: JC5520 R; Kohen, R.; Metcalf, M.A.; Khan, N.; Druck, T.; Hue J. Neurochem. 66, 47-56, 1996 A; Title: Cloning, characterization, and chromosomal A; Reference number: JC5520; MUID:96102917 A; Accession: JC5520

#sequence\_revision 05-Sep-1997 #text\_change 05-Nov-1999

(5-HTR6)

T.; Huebner, K.; Lachowicz, J.E.;

Meltze

localization of a human 5-HT 6 se

serotonin receptor 6 - human

A; Residues: 1-440 < KOH> A; Molecule type: mRNA

high affinity for several therapeutically important

ant

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A;Map position: 1p35-36
A;Introns: 238/3; 291/3
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein coupled receptor; glycoprotein; neurot
E;Reywords: G protein coupled receptor; glycoprotein; neurot
F;28-51/Domain: transmembrane #status predicted <TM1>
F;65-88/Domain: transmembrane #status predicted <TM2>
F;100-123/Domain: transmembrane #status predicted <TM3>
F;143-166/Domain: transmembrane #status predicted <TM4>
F;185-208/Domain: transmembrane #status predicted <TM5>
F;266-289/Domain: transmembrane #status predicted <TM5>
F;269-321/Domain: transmembrane #status predicted <TM7>
F;10/Binding site: carbohydrate (Asn) (covalent) #status pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:L41147; NID:g1162923; PIDN:AAA92622.1; PID:g1162924 A;Experimental source: brain C;Comment: This protein shows high affinity for several therapeutically im C;Genetics:
A;Gene: HTR6
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C; Species: Ratt
C; Date: 02-Aug
C; Accession: IS
R; Monsma, F.J.
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A;Title: Cloning and expression of a novel
A;Reference number: I57942; MUID:93196608
A;Accession: I57942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:L03202; NID:g294507; PIDN:AAA40618.1; PID:g294508 C;Superfamily: vertebrate rhodopsin
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376; Conserv
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A;Title: A novel rat serotonin (5-H76) receptor: molecular cloning, localization A;Reference number: JN0591; MUID:93277562
A;Molecular type: 100-2009
A;Molecula
A; Molecule type: DNA
A; Residues: 1-466 < JAS>
A; Cross-references: EMB
                                                                                                                                                                                                                                                beta-1-adrenergic receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 09-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 13-Aug-1999
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S36794
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N;Alternate names: 5-hydroxytryptamine receptor 6 (5-HTR6)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Nov-1999
C;Accession: JN0591
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JN0591
                                                                                                A; Reference number: S36794; A; Accession: S36794
                                                                                                                                                    Biochim. Biophys. Acta 1178, 307-309, 19 A; Title: Primary structure of the mouse
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A; Introns: 238/3
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A; Residues: 1-436 < RUA>
                                                                         A; Status: preliminary
                                                                                                                                                                                                      R;Jasper,
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                                                                                                                                                                                                                                                                                                                                                                                                                                    J.R.; Link, R.E.;
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Le names: 5-hydroxytryptamine receptor
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  EMBL:L10084;
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91.7%;
                                                                                                                  רוe mouse beta(1)-adrenergic receptor
MUID:93372116
                                                                                                                                                                                                   Chruscinski, A.J.;
  NID:g293278;
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Pred. No. 1.3e
6; Mismatches
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.3e-122;
     PIDN:AAA02929
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PID:g293279
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R; Shinomura, H.; Terada, A.

submitted to the EMBL Data Library, July 1991

A; Reference number: $40185

A; Accession: $40185

A; Molecule type: DNA

A; Residues: 1-25, 'A', 26-174, 'R', 175-464 <SH2>

A; Cross-references: EMBL:D00634; NID:9220670; PIDN:BAA00527.1; PID:9

A; Cross-references: EMBL:D00634; NID:9220670; PIDN:BAA00527.1; PID:9

A; Rachida, C.A.; Bunzow, J.R.; Searles, R.P.; Van Tol, H.; Tester, E

R; Machida, C.A.; Bunzow, J.R.; Searles, R.P.; Van Tol, H.; Tester, E

A; Rachida, C.A.; Bunzow, J.R.; Searles, R.P.; Van Tol, H.; Tester, E

A; Hachida, C.A.; Bunzow, J.R.; Searles, R.P.; Van Tol, H.; Tester, E

A; Hachida, C.A.; Bunzow, J.R.; Searles, R.P.; Van Tol, H.; Tester, E

A; Machida, C.A.; Bunzow, J.R.; Searles, R.P.; Van Tol, H.; Tester, E

A; Reference number: A36618; MUID:90330633

A; Accession: A36618

A; Residues: 1-26, 'A', '27-160, 'L', 162-174, 'R', 175-264, 'T', 266-464 <MAC

A; Cross-references: GB:J05561; NID:9203073; PIDN:AAA40792.1; PID:921

C; Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    beta-1-adrenergic receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change
C;Accession: S12591; S40185; A36618
R;Shimomura, H.; Terada, A.
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A:Residues: 1-464 <SHI>
A:Cross-references: EMBL:D00634
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C;Keywords: G protein-coupled receptor; phosphoprotein;
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Pred. No. 2.1e-38;
3; Mismatches 154;
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C; ACCESSALOR NIPPER, V.DRA Seq. 4, 231-241, 1994
A; Title: The rhesus macaque
A; Title: The umber: I53053;
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A;Molecule type: DNA
A;Residues: 1-480 <RES>
A;Cross-references: EMBL:X75540; NID:Q
C;Superfamily: vertebrate rhodopsin
C;Keywords: neurotransmitter receptor
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C;Date: 02-Jul-1996 #sequence_revision 02-
C;Accession: I53053
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                                                                                                                                                      1 MVPEPGPTANSTPAWGAGPPSAPGGSGWVAA---ALCVVIALTAAANSLLIALICTQPAL
                CLISLDRYLLILSPLRYKLRMTPLRALALVLGAWSLAALASFLPLLLLGW--HELGHARPP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCNGGTTTVDSDSSLDEPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLVSLFTSDLMVGLVVMPPAMLNALYGRWVLARGLCLLWTAFDVMCCSASILNLCLISLD 123
CVIALDRYLAITSPFRYQSLLTRARARGLVCTVWAISALVSFLPILMHWWRAESDEARRC
                                                            OTLTNLFIMSLASADLVMGLLVVPFGATIVVMGRWEYGSFFCELWTSVDVLCVTASIETL
                                                                                          RNTSNFFLVSLFTSDLMVGLVVMPPAMLNALYGRWVLARGLCLLWTAFDVMCCSASILNL 117
                                                                                                                         LVP-ASPPASLLPPASEGP--EPLSQQWTAGMGLLMALIVLLIVAGNVLVIVAIAKTPRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---SGGSSGLRLTAQLLLPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRERQASLASPSLRTSHSGPRPGLS--LQQVLPLPLP--PDSDSDSDAG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NVVKAFHRDLVPDRLFVFFNWLGYANSAFNPIIYCRSP----DFRKAFQRLLCCARRAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIVQAV-CDCISPGLEDVLTWLGYCNSTMNPIIY---PLEMRDFKRALGRELPCPR---C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APSPSPGPPRPADSLANGRSSKRRPSRLVALREQKALK---TLGIIMGVFTLCWLPFFLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETLQVPRTPRPGVESADSR------RLATKHSRKALKAKLTLGILLGMFFVTWLPFFVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDFVTNRAYAIASSVVSFYVPLCIMAFVYLRVFREAQKQVKKIDSCERKFLSGPPRPPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRLLASLPFVLVASGLTFFLPSGAICFTYCRILLAARKQAVQVASLTTGMAS-----QAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RYLAITSPERYQSLLTRARA-ALVCTVWAISALVSFLPILMHWWRAESDEARRCYNDPKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RYLLILSPLRYKLRMTPLRALALVLGAWSLAALASFLPLLLGW--HELGHARPPV--PGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPASLLPPASEG - - SAPLSQQWTAGMGLLLALIVLLIVVGNVLVIVAIAKTPRLQTLTNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTANSTPAWGAGPPSAPGGSGWVAA---ALCVVIALTAAANSLLIALICTQPALRNTSNF
                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----RAAH-GDRPRASGCLARAGPPPSPGAPSDDDDDDAGATPPARLLEPW 434
                                                                                                                                                                                                                                                                                            EMBL: X75540; NID: g510532; PIDN: CAA53228.1;
                                                                                                                                                                                                                                                                                                                                                                                                                         V.J.; Machida,
                                                                                                                                                                                                      24.6%;
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35.5%;
                                                                                                                                                                                                                                                                                                                                                                            beta 1-adrenergic MUID:95078456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63;
                                                                                                                                                                                     62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 581; DB 2; Pred. No. 1.4e-37;
                                                                                                                                                                                                      Score 563.5; DB 1
Pred. No. 3.2e-36;
                                                                                                                                                                                                                                                                                                                                            from GB/EMBL/DDBJ
                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 155;
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                                                                                                                                                                                                                                                                                                                                                                                                                            C.A.
                                                                                                                                                                                                                                                                                                                                                                                             receptor
                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                       166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        #text_change 13-Aug-1999
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                                                                                                                                                                                                                      480;
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                                                            149
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F;34-121/Domain: transmembrane #status predicted <TM2>
F;133-154/Domain: transmembrane #status predicted <TM3>
F;177-199/Domain: transmembrane #status predicted <TM4>
F;224-245/Domain: transmembrane #status predicted <TM5>
F;325-346/Domain: transmembrane #status predicted <TM6>
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A;Title: Cloning of the cDNA for the human beta-1-adrenergic
A;Reference number: A39911; MUID:88068509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    beta-1-adrenergic receptor - human
c;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 18-Aug-1995 #text_change 22-Jun-1999
C;Accession: A39911
R;Frielle, T; Collins, S.; Daniel, K.W.; Caron, M.G.; Lefkowitz, R.J.; Kob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
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A; Residues: 1-477 <FRI>
A; Cross-references: GB:J03019;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Keywords: G protein-coupled receptor; glycoprotein;
F;58-84/Domain: transmembrane #status predicted <TM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: 10q25-10q25
C; Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: GDB: ADRB1; ADRB1R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: A39911
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58-84/Domain: transmembrane #status predicted <TMl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     358-377/Domain: transmembrane #status predicted <TM7> 15/Binding site: carbohydrate (Asn) (covalent) #status
                       233
                                                                213
                                                                                                         177
                                                                                                                                              153
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                                                                                                                                                                                                                                  93
                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                  33
                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 144; Conserv
                                                                                                                                            LVPASPPASLLPPASESPEPLSQQWTAGMGLLMALIVLLIVAGNVLVIVAIAKTPRLQTL 92
                                                                                                                                                                                                                                                                                                                                                         MVPEPGPTANSTPAWGAGPPSAPGGSGWVAAALCVVIALTAAANSLLIALICTQPALRNT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DAGSGGSSGLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MRDFKRALGRFLPCPRCPRERQASLASPSLRTSHSGPRPGLSLQQVLPLPLP-PDSDSDS
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                       ASET -----
                                                                                                                                                                                                                              TNLFIMSLASADLVMGLLVVPFGATIVVWGRWEYGSFFCELWTSVDVLCVTASIETLCVI 152
                                                                                                                                                                                                                                                                     SNFFLVSLFTSDLMVGLVVMPPAMLNALYGRWVLARGLCLLWTAFDVMCCSASILNLCLI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -TLGIIMGVETLCWLPFFLANVVKAFHRELVPDRLFVFFNWLGYANSAFNPIIYCRSP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YNDPKCCDFVTNRAYAIASSVVSFYVPLCIMAFVYLRVFREAQKQVKKIDSCERRFLGGP
                                                            PKCCDFVTNRAYAIASSVVSFYVPLCIMAFVYLRVFREAQKQVKKIDSCERRFLGGPARP 272
                                                                                                 PGQCRLLASLPFVLVASGLTFFLPSGAICFTYCRILLAARKQAVQVAS----LTTGMASQ 232
                                                                                                                                                                                     SLDRYLLILSPLRYKLRMTPLRALALVLGAWSLAALASFLPLLLGW--HELGHARPPV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDVVGATQPARL 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTLGILLGMFFVTWLPFFVANIVQAV-CDCISPGLFDVLTWLGYCNSTMNPIIY---PLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --DFRNAFQRLLCCARRAARRRHAAHGDRPRASGCLARPG-----PPPSPGAASDDDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transmembrane #status predicted <TM4>
transmembrane #status predicted <TM5>
transmembrane #status predicted <TM6>
transmembrane #status predicted <TM7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDB:119654; OMIM:109630
  -LQVPRTPRPGVESADS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         394
                                                                                                                                                                                                                                                                                                                                                                                                                      24.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NID:g178199;
                                                                                                                                                                                                                                                                                                                                                                                                  67;
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 557; DB 1
Pred. No. 1e-35;
                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIDN: AAA51667.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 477;
                                                                                                                                                                                                                                                                                                                                                                                                  169;
RRLATKHSRKALKAKLTLGIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---RRLATKHSRKALKAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                   273
                                                                                                                                            212
                                                                                                                                                                                     176
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                                                                                                                                                                   В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; n:
C;Keywords: G protein-coupled receptor; glycoprotein; n:
F;37-63/Domain: transmembrane #status predicted <TM1>
F;73-101/Domain: transmembrane #status predicted <TM3>
F;113-133/Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Stoffel, B.; Meyer, H.H.D. submitted to the EMBL Data Library, June 1992 submitted to Boyine beta3-adrenergic receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          beta-3-adrenergic receptor - bovine (Species: Bos primigenius taurus (cattle) (C;Species: Bos primigenius taurus (cattle) (C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Aug-1999 (C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Aug-1999 (C;Accession: S65459; S40504; S31659 R;Pietri-Rouxel, F.; Lenzen, G.; Kapoor, A.; Drumare, M.F.; Archimbault, P.; Strosber Bur. J. Biochem. 230, 350-358, 1995 Bur. J. Biochem. 230, 350-358, 1995 A;Reference number: S65459; MUID:95324546 A;Accession: S65459; MUID:95324546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 4-5, 'HE', 8-105 <STO>
A; Cross-references: EMBL: X67214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X85961; NID:g757758; PIDN:CAA59937.1; PID:g757759 A;Experimental source: brown adipose tissue R;Casteilla, L.; Muzzin, P.; Revelli, J.P.; Ricquier, D.; Giacobino, J.P. Biochem. J. 297, 93-97, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: S31659
A; Accession: S31659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: S40503; MUID: 94107292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Expression of beta(1)- and beta(3)-adrenergic-receptor messages and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 162-298 < CAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S40504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ite fat
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 143; Conserva
     120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           439 TPPARL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  389
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                                                            71
                                                                                                                60
                                                                                                                                                                      11
                                                         MTNVFVTSLATADLVVGLLVVPPGATLALTGHWPLGVTGCELWTSVDVLCVTASIETLCA 130
                                                                                                                                                                   LTPWPDIPTLAPNTANASGLPGVPWAVALAGALLALAVLATVGGNLLVIVAIARTPRLQT 70
                                                                                                                                                                                                                       MVPEPG-PTANSTPAWGAGPPSAPGGSGWVAAALCVVIALTAAANSLLIALICTOPALRN 59
                                                                                         TSNFFLVSLFTSDLMVGLVVMPPAMLNALYGRWVLARGLCLLWTAFDVMCCSASILNLCL 119
ISLDRYLLILSPLRYKLRMTPLRALALVLGAWSLAALASFLPLLLGWHELG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALGRELPCPRCPRERQASLASPSLRTSHSGPRPGLSLQQVLPLPLP-PDSDSDSDAGSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGVFTLCWLPFFLANVVKAFHRELVPDRLFVFFNWLGYANSAFNPITYCRSP----DFRK 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSPSPSPVPAPAPPPPGPPRPAAAAATAPLANGRAGKRRPSRLVALREQKALK - - - TLGII 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGMFFVTWLPFFVANIVQAV-CDCISPGLFDVLTWLGYCNSTNNPIIY---PLFMRDFKR 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1-405 <PIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  394
                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                             24.2%;
                                                                                                                                                                                                                                                                              61;
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                                                                                                                                                                                                                                                                              Score 554; DB 2;
Pred. No. 1.5e-35;
1; Mismatches 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          compared
                                                                                                                                                                                                                                                                                156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   partial genomic
                                                                                                                                                                                                                                                                                                                                 Length 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neurotransmitter receptor;
                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                              66;
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A;Map position: 8A2-4
A;Introns: 388/2
C;Superfamily: vertebr:
C;Keywords: G protein-
F;37-60/Domain: transm
                                                                                                                                                                                                                                         C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; glycoprotein;
F; 37-60/Domain: transmembrane #status predicted <TM1>
F; 70-98/Domain: transmembrane #status predicted <TM2>
F; 110-130/Domain: transmembrane #status predicted <TM3
F; 153-176/Domain: transmembrane #status predicted <TM3
F; 101-222/Domain: transmembrane #status predicted <TM4
F; 201-222/Domain: transmembrane #status predicted <TM6
F; 290-311/Domain: transmembrane #status predicted <TM6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X72862; NID:g298112; PIDN:R;van Spronsen, A.; Nahmias, C.; Krief, S.; Briend-Eur. J. Biochem. 213, 1117-1124, 1993
A;Title: The promoter and intron/exon structure of A;Reference number: S32826; MUID:93279311
A;Accession: S32827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Species: Mus musculus (house mouse)
C; Date: 03-Feb-1994 #sequence_revision
C; Accession: S32804; S32827; S18548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δã
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-8;341-347;380-400 <SPR>
R; Nahmias, C.; Blin, N.; Elalouf, J.M.; Mattei, M.G.;
EMBO J. 10, 3721-3727, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: S18548; MUID:92037534
A;Accession: S18548
MOLecule type: DNA
Residues: 1-388 <NAH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Emorine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      beta-3-adrenergic receptor -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X60438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Title: Molecular characterization of the
                                                                                                                                                                                              290-311/Domain: transmembrane #status
324-344/Domain: transmembrane #status
;8,26/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics:
                                                                                                 Query Match
Best Local
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                                                                           Local Sin
                              G
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PGPTANSTPA-WGAGP---PSAPGGSG-----WVAAALCVVIAL-TAAANSLLIALICTQ 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPEEHLAAASPPRAPS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARPPVPGQCRLLASLPFVLVASGLTFFLPSGAICFTYCRILLAARKQAVQVASLTTGM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LP------CPRCPRERQASLASPSLRTSHSGPRPGLSLQQVLPLPLPPDSDSDSDAGS 386
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                                                                                                 Similarity
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                                                                             Conservative
                                                                                                                                                                                                                transmembrane #status predicted <TM3>
transmembrane #status predicted <TM4>
transmembrane #status predicted <TM5>
transmembrane #status predicted <TM6>
transmembrane #status predicted <TM6>
transmembrane #status predicted <TM7>
                                                                                                 24.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GAPTALTSPAGPMQ---
                                                                             60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NID:g298112; PIDN:CAA51384.1; PID:g298113 Krief, S.; Briend-Sutren, M.M.; Strosberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NID: g50109; PIDN: CAA42966.1;
                                                                                                 Score 552.5; DB 2
Pred. No. 1.9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     March
                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-Feb-1994 #text_change 13-Aug-1999
                                                                                                                                                                                                 (covalent) #status
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                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   beta-3-adrenergic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strosberg, A.D.; Emorine,
                                                                                                                                                                                                                                                                                                                                                                                          transmembrane
                                                                           Indels
                                                                                                                        Length
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                                                                                                                                                                                                 predicted
                                                                                                                          400;
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                                                                        51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mouse beta3-adrenergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strosberg,
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                                                                        Gaps
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                                                                                                                                                                                       A:Cross-references: GDB:125240; OMIM:126449
A:Map position: 5q34-5q35
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein;
E:25-49/Domain: transmembrane #status predicted <TM1>
F:61-87/Domain: transmembrane #status predicted <TM2>
F:61-87/Domain: transmembrane #status predicted <TM2>
                                          F;98-119/Domain: transmembrane #status predicted <TM3>
F;140-163/Domain: transmembrane #status predicted <TM4>
F;194-214/Domain: transmembrane #status predicted <TM5>
F;2194-273/Domain: intracellular #status predicted <CYT5-
F;274-295/Domain: transmembrane #status predicted <TM6>
F;313-333/Domain: transmembrane #status predicted <TM7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X55760;
R;Sunahara, R.K.; Niznik, H.B.; V
Nature 347, 80-83, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
C;Accession: S11377; S11376; S11379
R;Zhou, Q,Y.; Grandy, D.K.; Thambi, L.; Kushner, J.A.; van Tol, H.H.M.; Con. Nature 347, 76-80, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
DYHUD1
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     F; 5, 175/Binding
F; 96-186/Disulf
                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-446 <SUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A; Accession: S11379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Human dopamine D(1) receptor encoded A; Reference number: S11379; MUID: 90370095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Molecular cloning and expression A; Reference number: S11376; MUID: 90370093 A; Accession: S11376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Dearry, A.; Gingrich, J.A.;
Nature 347, 72-76, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-446 <ZHO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Cloning and expression of human and A; Reference number: S11377; MUID:90370094 A; Accession: S11377
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                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA; mRNA
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  96-186/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIFSLCWLPFFLANVLRALAGPSLVPSGVFIALNWLGYANSAFNPVIYCRSPDFRDAFRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GRFLPCPRC---PRERQASLASPSLR--TSHSGPRP
                           site: carbohydrate (Asn)
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                           (covalent) #status
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Brann, M.R.;
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Caron, M

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Accession: A41679
Muzzin, P.; Revelli, J.P.; Kuhne, F.; Gocayne, J.D.; McCombie, W.R.; Vente J. Biol. Chem. 266, 24053-24058, 1991
A;Title: An adipose tissue-specific beta-adrenergic receptor. Molecular clon A; Reference number: A41679; MUID:92084710
A; Accession: A41679; MUID:92084710
A; Accession: A41679; MUID:92084710
A; Residues: 1-400 <MUIZ>
A; Cross-references: GB:M74716; NID:950087; PIDN:AAA74470.1; PID:9202766
A; Experimental source: brown adipose tissue
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
C; Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
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C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 13-Aug-1999
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                         PRLQTITNVFVTSLATADLVVGLLVMPPGATLALTGHWPLGATGCELWTSVDVLCVTASI 122
                                                              PALRNTSNFFLVSLFTSDLMVGLVVMPPAMLNALYGRWVLARGLCLLWTAFDVMCCSASI 114
                                                                                                        PWPHKNGSLAFWSDAPTLDPSAANTSGLPGVPWAAALAGALLALATVGGNLLVITAIART
                                                                                                                                               PGPTANSTPA-WGAGP---PSAPGGSG-----WVAAALCVVIAL-TAAANSLLIALICTQ
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                                                                                                                                                                                                         24.1%; Score 551.5; 35.8%; Pred. No. 2.
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Pred.
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                                                                                                                                                                                     Mismatches
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No. 2.1e-35;
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A; Residues: 1-400 <BEN>
A; Cross-references: GB:S56481; NID:g298306; PIDN:AAB25520.1; PID:g298307
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross references: GB:S73473; NID:g241215; PIDN:AAB20702.1; PID:g241216 A;Note: sequence extracted from NCBI backbone (NCBIN:73473, NCBIP:73476) R;Bensaid, M.; Kaghad, M.; Rodriguez, M.; le Fur, G.; Caput, D. FEBS Lett. 318, 223-226, 1993 A;Title: The rat beta3-adrenergic receptor gene contains an intron. A;Reference number: S29808; MUID:93178631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 C;Accession: A53281; S29808 R;Granneman, J.G.; Lahners, K.N.; Chaudhry, A. Mol. Pharmacol. 40, 895-899, 1991 A;Title: Molecular cloning and expression of the ra A;Reference number: A53281; MUID:92100057
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A;Status: preliminary
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A; Residues: 1-400 <GRA>
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                     w
                                                                                                                                                                                                                                                                                                                                                        5 PGPTANSTPA-WGAGP---PSAPGGSG-----WVAAALCVVIAL-TAAANSI,LIALICTQ
                                                                                                                                                                                     LNLCLISLDRYLLILSPLRYKLRMTPLRALALVLGAWSLAALASFLPLLLGWHELG----
                                                                                                                                                                                                                                                 AL----GRFLPCPRC---PRERQASLASPSLR--TSHSGPRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GIFSLCWLPFFLANVLRALVGPSLVPSGVFIALNWLGYANSAFNPLJYCRSPDFRDAFRR
                                          TGMASQASETLQVPRTPRP---
                                                                                                             ----HARPPVPGQCRLLASLPFVLVASGLTFFLPSGAICFTYCRILLAARKQAVQVASLT
                                                                                                                                                                  ETLCALAVDRYLAVTNPLRYGTLVTKRRARAAVVLVWIVSATVSFAPIMSQWWRVGADAE 182
                                                                                                                                                                                                                                                                       PALRNTSNFFLVSLETSDLMVGLVVMPPAMLNALYGRWVLARGLCLLWTAFDVMCCSASI 114
                                                                                                                                                                                                                                                                                                                                     PWPHKNGSLAFWSDAPTLDPSAANTSGLPGVPWAAALAGALLALATVGGNLLVITAIART
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GREPPEESPRSPSRSPSPATVGTP-TASDGVPSCGRRPARLLPLGEHRALR---TLGLIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----HARPPVPGQCRLLASLPFVLVASGLTFFLPSGAICFTYCRILLAARKQAVQV----
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                                                                                     AQECHSNPRC---CSFASNMPYALLSSSVSFYLPLLVMLFVYARVFVVAKRQR-RLLRRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQECHSNPRC---CSFASNMPYALLSSSVSFYLPLLVMLFVYARVFVVAKRQRRFVRREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Norway rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       24.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 551.5; DB 2;
Pred. No. 2.3e-35;
1; Mismatches 148;
                       -GVESADSR--RLATKHSRKALKAKLTLGILL
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3-adrenergic receptor

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51;

Gaps

15;

62 54

274 238

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R;Lowe, A.L.; Walston, J.; Shuldiner, A.R. submitted to the EMBL Data Library, July 1996 A;Reference number: H01989 A;Accession: G02953 A;Status: preliminary; translated from GB/EMBL/DDBJA;Status: preliminary;
  A; Molecule type: DNA
A; Residues: 1-418 <LOW>
A; Cross-references: EMBI
                                                                                                                                                                           beta-3-adrenergic receptor - rhesus macaque C;Species: Macaca mulatta (rhesus macaque) C;Date: 21-Dec-1996 #sequence_revision 06-J-C;Accession: G02953
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A; Residues: 1-363 <FRA>
A; Cross-references: GB:L08602; NID:g212949;
C; Superfamily: vertebrate rhodopsin
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A;Accession: 150475
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Title: Cloning and characterization of a truncated dopamine D1 receptor from goldfish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dopamine D1 receptor - goldfish
C;Species: Carassius auratus (goldfish)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Aug-1999
C;Accession: I50475
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C; Keywords: neurotransmitter receptor
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                                                                                                                                                                                                                                                                                                                                                                                              STMNPIIYPLFMRDFKRALGRFLPCPR-CPRERQASLASPSL 353
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127; Conserv
EMBL: U63592; NID: g1458230; PIDN: AAB53939.1; PID: g1458232
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Pred. No. 4.1e-35;
53; Mismatches 119;
                                                                                                                                                                                                  macaque)
ision 06-Jun-1997
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C; Genetics:
A; Introns:
C; Superfami
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C; Keywords:
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Am. J. Physiol. 268, F423-F434, 1995
A;Title: Cloning of the porcine DIA dopamine receptor
A;Reference number: 147217; MUID:95208810
A;Accession: 147217
                                                                                                                                                                                                                                                                                                                                                                                                                                                            dopamine receptor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997
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A; Residues: 1-446 <GRE>
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Best Local
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69 FTSDLMVGLVVMPPAMLNALYGRWVLARGLCLLWTAFDVMCCSASILNLCLISLDRYLLI 128
                                                                                           21 SAPGGSGWV----
                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 LVPWPDVPTLAPNTANTSGLPGVPWAAALAGALLALAVLATVGGNLLVIVALTRTPRLQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                       7 STMDGTGLVVERDFSFRILTACFLSLLILSTLLGNTLVCAAVIRFRHLRSKVTNFFVISL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MYPEPG-PTANSTPAWGAGPPSAPGGSGWVAAALCVVIALTAAANSLLIALICTQPALRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TWLPFFVANIVQAVCDCISPGL----FDVLTWLGYCNSTMNPIIY---PLFMRDFKRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEESSPALSRSLAPAPAGTCAPPEGVPACCRRPARLLPLREHRAL - - - CTLGLIMGTFTL
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Pred. No. 2.6e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 543.5; DB 2
Pred. No. 9.8e-35;
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418 P-----ALSVILDYDTDVSLEKIQPITQNGQHP 445
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                                            236 TLQVPRTPRPGVESADSRRLATKHSRKALKAKLTLGILLGMFFVTWLPFFVANIVQAVCD 295
                                                                                                                                                                                183 THNCDSSLSRTYAISSSLISFYIPVAIMIVTYTRIYRIAQKQIRRISALERAAVHAKNCQ 242
                                                                                                                                                                                             179 --OCRILLASLPEVLVASGLTFFLPSGAICFTYCRILLAARKQAVQVASL-TTGMASQASE 235
                                                                                                                                                                                                                                                                         67 AVSDLLVAVLVMPWKAVAEIAGFWPFG-SFCNIWVAFDIMCSTASILNLCVISVDRYWAI 125
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Search completed: March 15, 2002, 14:10:49 Job time: 114 sec

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Minimum DB
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Copyright (c) 1993 - 2000 Compugen Ltd.
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09crr2 mus musculu
09g156 ovis aries
09gj56 ovis aries
09gj50 ovis aries
09gj57 ovis aries
09gj57 ovis aries
09g157 ovis aries
04g198 apis mellif
09mz00 sus scrofa
098841 anguilla an
042315 cyprinus ca
096716 branchiosto
098842 anguilla an
09gw71 rattus sp.
09ng02 apis mellif
09ttm9 sus scrofa
098844 anguilla an
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19.6	19.7	19.7	19.7	19.8	19.8	19.9	20.0	20.0	20.0	20.1	20.2	20.2	20.3	20.4	20.6	20.6	21.0	21.1	21.1	21.2	21.3	21.3	21.3	21.4	21.4	
455	429	425	377	471	408	466	499	429	358	397	359	466	464	466	394	470	508	515	518	384	458	419	394	392	380	
4	6	σ	6	11	13	4	4	4	11	11	4	6	5	11	5	11	σ	11	σ	13	13	ر.	G	13	13	
060451	Q9MZU3	Q9MZU2	Q9N263	Q9QW77	866860	Q9UD63	Q13675	Q13729	Q9QX37	Q9D282	Q9н199	Q9TSW7	Q9GQ54	Q9WU25	Q9NJS6	P97842	Q9VCZ3	Q9DBL0	09MY18	042318	Q98843	077254	Q9NHF3	Q9YHA5	042317	
060451 homo sapien	Q9mzu3 oryctolagus	Q9mzu2 oryctolagus	Q9n263 sus scrofa	Q9qw77 cricetulus	Q98998 xenopus lae	Q9ud63 homo sapien	Q13675 homo sapien	Q13729 homo sapien	Q9qx37 mus musculu	Q9d282 mus musculu	Q9h199 homo sapien		Q9gq54 aedes aegyp	Q9wu25 cavia porce	Q9njs6 aplysia kur	P97842 rattus norv	Q9vcz3 drosophila	Q9dbl0 mus musculu	Q9myi8 oryctolagus	O42318 cyprinus ca	Q98843 anguilla an	077254 boophilus m	Q9nhf3 aplysia cal	Q9yha5 myxine glut	042317 cyprinus ca	

## ALIGNMENTS

Qy	Qу	Qи Ве <b>м</b> а	SQ	DR DR	DR DR	DR DR	38	CC RL	R R T	RA	RA S	R R	RP	R OX	8	8	S E	DI	Ŋ	AC ID	263004	RESULT
61 SNFFLVSLFTSDLMVGLVVMPPAMLNALYGRWVLARGLCLLWTAFDVMCCSASILNLCLI 120	1 MVPEPGPTANSTPAWGAGPPSAPGGSGWVAAALCVVIALTAAANSLLIALICTGPALKNT 60          :	Query Match  88.4%; Score 2025; DB 11; Length 438; Best Local Similarity 88.9%; Pred. No. 4.3e-136; Matches 391; Conservative 12; Mismatches 35; Indels 2; Gaps 1;	n coupled receptor; Glycoprotei 438 AA; 46786 MW; DB904038	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1. PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.	Pfam; PF00001; 7tm_1; 1. PRINTS; PR00237; GPCRRHODOPSN.	InterPro; IPR000276; GPCR_Rhodpsn.		J. Neurochem. 66:47-56(1996). -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).	"Cloning, characterization, and chromosomal localization of a human 5-HT6 serotonin receptor.";		Kohen R., Metcalf M.A., Khan N., Druck T., Huebner K., Lachowicz J.E.,	STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN STRIATUM; MEDITNE=96102917: DibMod=8522988:	SEQUENCE FROM N.A.	NCBI_TaxID=10116;	a; Rodentia; Sciurognathi; Muridae;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	5-HT6 SEROTONIN RECEPTOR.	01-NOV-1990 (TEMBLEEL 01, Last sequence update) 01-JUN-2001 (TrEMBLEEL 17, Last annotation update)	1996 (Tremburel, 01, Creat	Q63004 PRELIMINARY; PRT; 438 AA.		LT 1

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A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Ba Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Ra Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ra Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

Ra Kuehi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ra Kuehi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ra Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Ra Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Ra Blake J., Boifelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Ra Blake J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Ra Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Ra Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Ra Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Ra Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Ra Havashizaki Y.:
                      -!- SIMILARITY: BELONGS TO FAMILY EMBL; AKO18378; BAB31185.1; -. MGD; MGI:87937; Adrbl.
InterPro; IPR000276; GPCR_Rhodpsn. pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODDPSN.
                                                                                                                                                                                             Nature 409:685-690(2001).
-!- SUBCELLULAR LOCATION: INTEGRAL
     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                              "Functional annotation of a full-length mouse
                                                                                                                                                                                                                                                                                 Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9CRR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RTPRPGVESADSRRLATKHSRKALKAKLTLGILLGMFFVTWLPFFVANIVQAVCDCISPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-EMBRYONIC LUNG;
G_PROTEIN_RECEP_F1_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BETA 1
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(FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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The J., Fukuda :
                                                                                                                                                                   COUPLED
                                                                                                                                                                                                                                                    collection.";
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Query Match Best Local S Matches 146

Similarity

24.6%; 34.8%;

Score 563.5; Pred. No. 1.

.7e-32;

DΒ

405;

146;

Conservative

56;

Mismatches

163; 6,

Indels Length

55,

Gaps

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Best Local (
                                                                                                                                                                                                                                                                                                    Q9GL56 PRELIMINARY;
Q9GL56;
01-MAR-2001 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
BETA 3 ADRENERGIC RECEPTO
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Glycoprotein; Receptor; T
G-protein coupled receptor; Glycoprotein; Receptor; T
SEQUENCE 405 AA; 42886 MW; EF4B13BB413EA413 CRC64
                                                       SEQUENCE FROM N.A.
FORTEST R.H., HICKFORD J.G.H.;
PROTEST R.H., HICKFORD J.G.H.;
"POLYMORPHISM WITHIN the ovine beta 3 adrenergic receptor of the EMBL/GenBank/DDBJ databases."
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY I.SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED EMBL; AF314203; AAG31166.1;
Interpro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00027, GPCRRHODDPSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Glycoprotein; Transmembrane
NON_TER 1 1
                                                                                                                                                                                                                                Ovis aries (Sheep).
Eukaryota; Metažoa; Chordata; Craniat
Mammalia; Eutheria; Cetartiodactyla;
Boyidae; Caprinae; Ovis.
                                                                                                                                                                                                                   NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVLPLPLP--PDSDSDSDAG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NPIIY---PLEMRDFKRALGRELPCPR---CPRERQASLASPSLRTSHSGPRPGLS--LQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALREQKALK---TLGIIMGVFTLCWLPFFLANVVKAFHRDLVPDRLFVFFNWLGYANSAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TKHSRKALKAKLTLGILLGMFFVTWLPFFVANIVQAV-CDCISPGLFDVLTWLGYCNSTM
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                                                                                                                                                                                                                                                                                                        RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44741 MW;
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36.5%;
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16,
17,
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                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
actyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                    G-PROTEIN COUPLED
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                                                                                                                                                         receptor gene.";
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                Transmembrane
                                                                                                                                 SIMILARITY)
                                                                                                                    RECEPTORS
                                                                                                                                                                                                                                                 Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                402
                                                                                                                                                                                                                                                                                                                                                                                                                                                      395
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"Polymorphism within the ovine beta 3 adrenergic recepto:
submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY 9-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED EMBL; AF314204; AAG31167.1; -.
EMBL; AF314204; AAG31165.1; -.
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.

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Bovidae; Caprinae; Ovis.
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Pred. No. 3.2e-32;
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Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Glycoprotein; Receptor: Trisepportein and the coupled receptor of the c
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"Polymorphism within the owine beta 3 adrenergic receptor submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases -- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY -- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLEI
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eta 3 adrenergic receptor
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Best Local S
Matches 146
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INTERPRO: IPR000276; GPCR_Rhodpsn.

Pfam; PP00001; 7tm_1; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.

G-PROTEIN_COUPLED ROSITE; Receptor; Transcription Coupled receptor; Glycoprotein; Receptor; Transcription Coupled ROSITE; PS00264; ROSITE; RO
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FORTEST R.H., Hickford J.G.H.;

POLYMOTPHISM WITHIN the ovine beta 3 adrenergic receptor gene.",

"POLYMOTPHISM WITHIN the EMBL/GenBank/DDBJ databases.

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2001 (TrEMBLrel. 17,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
NCBI_TaxID-9940;
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-ASLTTGMASQASETLQVPRTPRPGVESADSR---RLATKHSRKALKAKLTLGILLG
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InterPro; IPRO00276; GPCR_Rhodpsn.
Pfam; PF00001; Thu.1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
G-PROTEIN_COUPLED receptor; Glycoprotein; Transm SEQUENCE 402 AA; 44554 MW; 0B1962DC7F6481DF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apis mellifera (Honeybee).
Eukaryota; Metazoa; Arthropoda;
Pterygota; Neoptera; Endopterygo
Apoidea; Apidae; Apis.
NCBI_TaxID=7460;
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01-JUN-1998
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-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Glycoprotein; Receptor; Tr G-protein coupled receptor; GS98382A9B38DD9 CRC64;
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Eukaryota; Metazoa;
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Pred. No. 7.1e-31;
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01-JAN-1998 (TrEMBLrel. 0
01-JAN-1998 (TrEMBLrel. 0
01-JUN-2001 (TrEMBLrel. 1
D1A3 DOPAMINE RECEPTOR.
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01-FEB-1997
01-FEB-1997
01-JUN-2001
   Cyprinus carpio (Common carp)
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii;
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Glycoprotein; Transm G-protein coupled receptor; Glycoprotein Transm SEQUENCE 445 AA; 49442 MW; 2A26D945DE39ACDD
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J. Biol. Chem. 272:2778-2787(1997).
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MEDLINE-97160583; PubMed-9006917;

MEDLINE-97160583; PubMed-9006917;

Cardinaud B., Coudouel S., Vincent J.D., Vernier P.;

Cardinaud B., Coudouel S., Vincent J.D., Vernier P.;

Carly emergence of three dopamine D1 receptor subtypes in vertebrates. Molecular phylogenetic, pharmacological, and criteria defining D1A, D1B, and D1C receptors in European
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Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; ?
Anguillidae; Anguilla.
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EMBL; U62918; AAC60067.1
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Pfam; PF00001; 7tm_1; 1.
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la; Craniata;
i; Teleostei;
                                                                                                                                       Created)
Last sequence
Last annument
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Last sequences that the control of the con
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Pred. No. 1.9e
61; Mismatches
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annotation
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; Vertebrata; Euto
; Anguilliformes;
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UPLED RECEPTORS.
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7;

; Craniata; Teleostei;

Vertebrata; Euteleostei;

Enteleostomi;

Ostariophysi;

8

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DRACE REPORT OF THE PROPERTY O
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Best Local S
Matches 123
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01-NOV-1996 (TremBLrel. 01, Last sequ
01-JUN-2001 (TremBLrel. 17, Last anno
DOPAMINE DI-LIKE RECEPTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q24038
Q24038;
                                                                         STRAIR-CANTON S; TISSUE-HEAD;
STRAIR-CANTON S; TISSUE-HEAD;
MEDLINE-95237365; pubMed-7720859;
Sugamori K.S., Demchyshyn L.L., McConkey F.,
"A primordial dopamine D1-like adenylyl cycli
Drosophila melanogaster displaying poor affir
FEBS Lett. 362:131-138(1995).
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Submitted (AUG-1997) to the EMBL/GenBJ databases.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

EMBL; Y14626: CAA74970.1;
InterPro; IPR000276; GPCR_Rhodpsn.

Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Trachez
Pterygota; Neoptera; Endopterygota; Dip
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                         DOPR OR CG9652
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Glycoprotein; Transmembrane.
SEQUENCE 446 AA; 49800 MW; 417834A303627D20 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly)
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NCBI_TaxID=7962;
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  SUBCELLULAR LOCATION: INTEGRAI SIMILARITY: BELONGS TO FAMILY L; U22106; AAA85716.1; -.
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01, Last sequence up
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                     INTEGRAL MEMBRANE PROTION OF FAMILY 1 OF G-PROTEIN
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                                                                                                 y F., Forte M.A., Niznik H cyclase-linked receptor fi affinity for benzazepines
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Matches
Interpro; IPKUUUZI, 1.

Pfam; PF00001; 7tm_1; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

AR707 MW; A44749475F2139CE CRC64;
                                                                                                                                                                                                                                                                                           042316;
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SEQUENCE
                                                                                            Cyprinus carpio (Common carp).
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Cyprininae;
                                                                                                                                                                                                                                              01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
D1A4 DOPAMINE RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Glycoprotein; NON_TER 1 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FlyBase; FBgn0011582;
InterPro; IPR000276; G
Pfam; PF00001; 7tm_1;
                                                                                                                                                                                     NCBI_TaxID=7962;
                                                                                                                                                       TISSUE=RETINA;
                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                              RSSAELEQV
                                                                                                                                                                                                                                                                                                                                                                                  RPGLSLQQV
                                                                                                                                                                                                                                                                                                                                                                                                          FNPIIYSIFNKEFRDAFKRILTMRNPWCCAQDVGNIHPRNSDRFITDYAAKNVVVMNSG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSRKAL---KAKLTLGILLGMFFVTWLDFFVANIVQAVC-DCISPGLFDVLTWLGYCNST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AIWLLAAFVSFVPISLGIH-----RPDQPLIFEDNGKKYPTCALDLTPTYAVVSSCISFY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YGRWVLARGLCLLWTAFDVMCCSASILNLCLISLDRYLLILSPLRYKLRMTPLRALALVL 148
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385 ‡
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35.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 525; DB
Pred. No. 8.5e
53; Mismatches
                                                                                                                                                                                                                                                          Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                       Craniata;
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                                                                                                                                                                                                   Cyprinus
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Similarity

Length 437;

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                                                                                                                                   Cardinaud B., Gibert JM., Sugamori K.S., Coudouel S.,
Vincent J.D., Niznik H.B., Vernier P.;

"The amphioxus Dl/beta receptor and the emergence of
adrenergic system.";

L. Submitted (APR-1998) to the EMBL/GenBank/DDBJ databas
EMBL; AJ005433; CAA06536.1; -

R. InterPro; IPR00276; GPCR_Rhodpsn.
R. InterPro; IPR002106; AA_ENA_ligase_II.
R. Ffam; PF00021, 7tm_1; 1.
R. Pfam; PF00001; 7tm_1; 1.
R. PROSITE; PS00237; GPCRRHODPSN.
R. PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
R. PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
                                                             Query
Best I
                                                  Matches
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                Branchiostoma
                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
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01-MAY-1999
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                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=7740;
                                                                                                                                                                                                                                                                                                                                                                                   DOPAMINE D1/BETA RECEPTOR
                                                                                                              SEQUENCE
                                                                                                                            Receptor
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TANSTEA-SVGSCFAPNPYSAGVQAVLGLITVILILLTVIGNVLVILAVTCHRKMRTVTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IY-AFNAGFRKAFSILLGCHRLCPGSNAIEIVSINNNGGPPSTSQYQPKGHVPKEGNNSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --TLSVIMGVFVCCWLPFFVLNCMVPFCNPNEGSDFFCISSTTFDVFVWFGWANSSLNPI
                                                             Similarity
                                                                                                                391
                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 10, Created)
(TrEMBLrel. 10, Last sequence up
(TrEMBLrel. 17, Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                  Conservative
                                                                                                                AΑ;
                                                                                                                                                                                                                                                                                                                                                          Chordata; Cephalochordata;
                                                                                                              42622 MW;
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                                                             22.8%;
36.3%;
                                                 58;
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                                                            Score
Pred.
                                                                                                              67A5AD944AFA3FBE CRC64;
                                                Mismatches
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                                                             523.5; DB 5;
No. 1.1e-29;
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                                                                                                                                Query Match
Best Local Similarity
Matches 118; Conserv
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Q98842;
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InterPro; IPR000276; GPCR_Rhodpsn.

InterPro; IPR000299; Peptidase_S8.

Pfam; PF00001; 7tm_1; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.

PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Glycoprotein; Transmembrane.

G-protein coupled receptor; Glycoprotein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                   Cardinaud B., Coudouel S., Vincent J.D., Vernier P.:
"Early emergence of three dopamine D1 receptor subtypes vertebrates. Molecular phylogenetic, pharmacological, an criteria defining D1A, D1B, and D1C receptors in Europea anguilla.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1997 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
DOPAMINE DIA2 RECEPTOR.
                                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 272:2778-2787(1997).
-!- SUBCELLULAR LOCATION: INTEGRAL |
-!- SIMILARITY: BELONGS TO FAMILY 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anguilla anguilla (European fi
Eukaryota; Metazoa; Chordata;
Actinopterygii, Neopterygii;
Anguillidae; Anguilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=97160583; PubMed=9006917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=7936;
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SLAALASFLPLLLGWHEL---
                                                                           LSSLIVSTLLGNTLVCAAVTKFRHLRSKVTNFFVISLAVSDLLVAILVMPWKAVTEVAGF
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                           WPFG-SFCNIWVAFDIMCSTASILNLCIISVDRYWAISSPFRYERKMTPKVAFVMISVAW
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                                                                                                                                Conservative
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                                                                                                                                            22.3%;
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a; Craniata;
Teleostei;
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Last sequence update)
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Pred.
-GHARPPVPGQCRLLASLPFVLVASGLTFFLPSG
                                                                                                                                 Mismatches
                                                                                                                                             511.5; DB 13;
No. 8.8e-29;
                                                                                                                                                                                                                                                                                                                                  MEMBRANE PROTEIN (BY S
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Anguilliformes;
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Matches 150
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Q9QW71;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence of the control of the control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Glycoprotein; Transmembrane.
SEQUENCE 559 AA; 59739 MW; 37CD9BD696D3A47D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-92100054; PubMed=1661838; Perez D.M., Piascik M.T., Graham R.M.; Perez D.M., Piascik M.T., Graham R.M.; Solution-phase library screening for the identification of rare clones: isolation of an alpha 1D-adrenergic receptor cDNA."; Mol. Pharmacol. 40:876-883(1991).

1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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fam; PF00001; 7tm_1; 1.
                                                                                                                   292
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                                                                                                                                                                                                                                                                                                                                182 CTISVDRYVGVRHSLKYPAIMIERKAAAILALLWAVALVVSVGP-LLGWKE-----PVP
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VLCWFPFFFVLPLGSIFPQIKPSEGVFKVIFWLGYFNSCVNPLIYPCSSREFKRAFLRLL
                            PDERFCGITEEVGYAIFSSVCSFYLPMAVIVVMYCRVYVVARS---TTRSLEAGIKREPG
                                                                                                                                                                                                                                                     GO---CRLLASLPFVLVASGLTFFLPSGAICFTYCRILLAARKQAVQVASLTTGMASQAS
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                                                                                                             KASEVVLRIHCRGARTSAKGYPGTQSSKGHTLRSSLSVRLLKFSREKKAAKTLAIVVGVF
                                                                                                                                          ETLQV------PRTPR---PGVESADSRRLATKHSRKAL-----KAKLTLGILLGME
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Rodentia;
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Last annotation update)
SUBTYPE ALPHA 1D, ALPHA
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Search completed: March 15, 2002, 14:14:06 Job time: 211 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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US-08-969-267B-4
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24

Query Match 24.3%; Score 557; DB 2; Length Best Local Similarity 33.8%; Pred. No. 9e-35; Matches 144; Conservative 67; Mismatches 169; Inde	US-08-390-000A-7 US-08-390-000A-7 US-08-390-000A-7 Sequence 7, Application US/08390000A Patent No. 5985583 Patent No. 5985583 Patent NFORMATION: Cloning and Expression of TITLE OF INVENTION: Gonadotropin-Releasing Hormone in TITLE OF INVENTION: A MEDIUM TYPE: Pennie & Edmonds LLP STREET: 1155 Avenue of the Americas CITY: New York STATE: NOW YORK STATE: NOW YORK COUNTRY: U.S.A.  COUNTRY: U.S.A.  ZIP: 10036-27111  COMPUTER READABLE FORM: MEDIUM TYPE: Ploppy disk COUNTRY: U.S.A.  COUNTRY: U.S.A.  ZIP: 10036-2711  COMPUTER READABLE FORM: MEDIUM TYPE: Patentin Release #1.0, Version #1.25 COMPUTER READABLE OCOMPATION  POERATING SYSTEM: DC-DOS/MS-DOS SOFTWARE: DATA: MEDIUM TYPE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION NUMBER: U.S/08/390,000A FILLING DATA: DATA: APPLICATION NUMBER: U.S/08/390,000A FILLING DATA: A.S.  ATTORNEY/AGENT INFORMATION:  PATENTAL STATES ON THE STATE ON	ALIGNMENTS	28 508 22.2 559 2 US-08-406-855A-20 29 508 22.2 559 3 US-09-206-899-20 30 503 21.9 572 1 US-08-334-698-2 31 503 21.9 572 1 US-08-428-932-2 32 503 21.9 572 1 US-08-722-001-30 34 503 21.9 572 1 US-08-722-001-30 35 503 21.9 572 2 US-08-722-001-32 36 503 21.9 572 2 US-08-44-354-2 37 503 21.9 572 2 US-08-244-354-2 38 503 21.9 572 3 US-08-244-354-2 39 499.5 21.8 501 2 US-08-722-001-14 40 499.5 21.8 501 2 US-08-722-001-14 499.5 21.8 501 2 US-08-672-001-14 499.5 21.8 501 2 US-08-675-582-9 42 499.5 21.8 501 2 US-08-6858A-19 43 499.5 21.8 501 2 US-08-6858A-19 44 494.5 21.6 478 4 US-09-292-0658-33 45 494.5 21.6 478 4 US-09-292-0658-33
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US-08-087-772A-16
US-08-087-772A-16
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                                                                                                                         TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO:
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APPLICANT: Emorine, Jean L.
APPLICANT: Etrosberg, Donny A.
TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine
TITLE OF INVENTION: Beta3-Adrenergic Receptor and Their Applications
                 MOLECULE TYPE:
                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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                                                FILING DATE: 21-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: LENZEN, APPLICANT: KAPOOR,
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OPERATING SYSTEM:
SOFTWARE: Patentl
                NAME: OBLON, NORMAN F REGISTRATION NUMBER:
                                                                                                                    APPLICATION NUMBER: 93 04670 FILING DATE: 21-APR-1993
                                                                                                                                                                    CLASSIFICATION:
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                                                                                                                                                                                                      APPLICATION NUMBER:
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REFERENCE/DOCKET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASET------LQVPRTPRPGVESADS------RRLATKHSRKALKAKLTLGIL 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLDRYLLILSPLRYKLRMTPLRALALVLGAWSLAALASFLPLLLGW--HELGHARPPV--
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                                                                                                                                                                                                                                                                                                                                                                                                  1755 S.
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                                                                                                                                                                                                                                          PatentIn
                                                                                                                                                                                                                                                          IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                    OBLON,
                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                        21-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                  N, SPIVAK, MCLELLAND, MAIER & NEUSTADT JEFFERSON DAVIS HIGHWAY, SUITE 400
NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARCHANA
NUCLEOTIDE SEQUENCES CODING FOR THE
BOVINE BETA3-ADRENERGIC RECEPTOR AND THEIR APPLICATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GERLINDA
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                                                                                                                                                                                                                                          Release #1.0,
                                                                                    PCT/FR94/00447
                                                                                                                                                                                                        US/08/351,473B
                24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67; Mismatches
6639-001-0x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 557; DB 1;
Pred. No. 9.2e-35;
                                                                                                                                                                                                                                        Version
PCT
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                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/08467559B Patent No. 5928890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 24.2%;
Best Local Similarity 33.6%;
Matches 143; Conservative 6
                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
                    APPLICANT: LI, YI TITLE OF INVENTION: NUMBER OF SEQUENCES:
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LENGTH: 405 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 ISLDRYLLILSPLRYKLRMTPLRALALVLGAWSLAALASFLPLLLGWHELG------H
 FILING DATE:
             APPLICATION NUMBER: US/08/467,559B
                                                                                                                                                 COUNTRY:
                                                                                                                                                                   STATE:
                                                                                                                                                                               CITY: WASHINGTON
                                                                                                                                                                                                STREET:
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGSSGL 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEESPPAPSRSGSPGLAGPCASPAGVPSYGRRPARLLPLREHRALR---TLGLIMGTFTL
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                                                                                                                                                                                             3: STERNE, KESSLER, GO
06-JUN-1995
                                                                                                                                                                                                                                                                  HUMAN AMINE RECEPTOR
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Pred. No. 1.3e-34;
1; Mismatches 156; Indels
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E, NW, SUITE 600
                                                #1.30
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                                                                                                                                                                                                                                    Sequence 5, Application US/08351473B Patent No. 5656440 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                   NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 CRLLASLPFVLVASGLTFFLPSGAICFTYCRILLAARKQAVQVAS----LTTGMASQAS- 234
                                                                       CITY: ARLINGTON
STATE: VIRGINIA
                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: not
TOPOLOGY: not rei
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                                                                                                     STREET:
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                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                NVVKAFHRDLVPDRLFVFFNWLGYANSAFNPIIYCRSP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RYLAITSPERYQSLLTRARARALVCTVWAISALVSELPILMHWWRAESDEARRCYNDPKC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIMSLASADLYMGLLVVPFGATIVVWGRWEYGSFFCELWTSVDVLCVTASIETLCVIALD
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                                                                      VIRGINIA
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                                                                                                     1755 S.
                                                                                                                                                                                                   LENZEN, GERLINDA
KAPOOR, ARCHANA
                                                        USA
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                                                                                                     N, SPIVAK, MCLELLAND, MAIER & NEUSTADT JEFFERSON DAVIS HIGHWAY, SUITE 400
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                                                                                                                                                                     NUCLEOTIDE SEQUENCES CODING FOR THE BOVINE BETA3-ADRENERGIC RECEPTOR AND THEIR APPLICATIONS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,

Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

CLASSIFICATION:

FILING DATE:

21-FEB-1995

US/08/351,473B

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Best Local Similarity
                                 APPLICANT: EMORINE, LOUIS APPLICANT: STROSBERG, Donny TITLE OF INVENTION: INTRON/I TITLE OF INVENTION: GENES STROUGHCES: 9
                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (703) 413-222
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR94/00447
FILING DATE: 21-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 6639-001-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (703) 413-3000
TELEPHONE: (703) 413-2220
TELEFAX: (703) 413-2220
CORRESPONDENCE ADDRESS:
ADDRESSEE: KECK, MAH
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                          356 LLCSYGGRGPEEPRAVTFPASPVEARQSPPLNRFDGYEGARP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 PRLQTITNVFVTSLAAADLVVGLLVMPPGATLALTGHWPLGETGCELWTSVDVLCVTASI 122
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                                                                                                                                                                                                                                                                                                                              AL----GRFLPCPRC---PRERQASLASPSLR--TSHSGPRP 362
                                                                                                                                                                                                                                                                                                                                                                      GIFSLCWLPFFLANVLRALAGPSLVPSGVFIALNWLGYANSAFNPVIYCRSPDFRDAFRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQECHSNPRC---CSFASNMPYALLSSSVSFYLPLLVMLFVYARVFVVAKRQR-HLLRRE 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           400 amino acids
                                                                                                   STROSBERG, Donny
                                                                                                                        EMORINE, Laurent; MARULLO, Stefano;
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    MAHIN & CATE
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                                                                                INTRON/EXON OF THE HUMAN AND
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Best Local Similarity
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APPLICATION NUMBER: 07/721,571
FILING DATE: 25-MAY-1990
PRIOR APPLICATION NUMBER: PCT/FR89/00918
APPLICATION NUMBER: PCT/FR89/00918
FILING DATE: 25-CAN-1989
ATTORNEY/AGENT INFORMATION:
NAME: Fleit, Martin; Gollin, Michael A.
REGISTRATION NUMBER: 16,900; 31,957
REGISTRATION NUMBER: 16,900; 31,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 789-3400
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MEDIUM TYPE: 3-1/2" diskette
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APPLICATION NUMBER: 08/11
FILING DATE: 08-SEPT-1993
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CURRENT APPLICATION DATA:
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CLASSIFICATION:
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LLCSYGGRGPEEPRAVTFPASPVEARQSPPLNRFDGYEGARP
                                  AL----GRFLPCPRC---PRERQASLASPSLR--TSHSGPRP
                                                                         {\tt GIFSLCWLPFFLANVLRALAGPSLVPSGVFIALNWLGYANSAFNPVIYCRSPDFRDAFRR}
                                                                                          GMFFVTWLPFFVANIVQAVC--DCISPGLFDVLTWLGYCNSTMNPIIY---PLFMRDFKR 329
                                                                                                                                                 LGRFSPEESPPSPSRSPSPATGGTPAAPDGVPPCGRRPARLLPLREHRALR---TLGLIM 295
                                                                                                                                                                                       TGMASQASETLQVPRTPRP------GVESADSR--RLATKHSRKALKAKLTLGILL 274
                                                                                                                                                                                                                                                           ----HARPPVPGQCRLLASLPFVLVASGLTFFLPSGAICFTYCRILLAARKQAVQVASLT 226
                                                                                                                                                                                                                                                                                                    ETLCALAVDRYLAVTNPLRYGTLVTKRRARAAVVLVWIVSAAVSFAPIMSQWWRVGADAE 182
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                                                                                                                                                                                                                                                                                                                                                                                                            PALRNTSNEFLVSLFTSDLMVGLVVMPPAMLNALYGRWVLARGLCLLWTAFDVMCCSASI 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGPTANSTPA-WGAGP---PSAPGGSG-----WVAAALCVVIAL-TAAANSLLIALICTQ 54
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amino acid
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35.1%;
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Pred. No. 1.7e-34;
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US-08-450-962-6

Sequence

6, Application US/08450962

Patent No.

GENERAL INFORMATION:
APPLICANT: EMORIN
APPLICANT: STROSE

STROSBERG,

Donny

EMORINE, Laurent; MARULLO, Stefano;

INTRON/EXON OF THE HUMAN AND

TITLE OF INVENTION:

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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Fleit, Martin; Gollin, Michael REGISTRATION NUMBER: 16,900; 31,957 REFERENCE/DOCKET NUMBER: 47078-042 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/I
FILING DATE: 25-7MA-1989
ATTORNEY/AGENT INFORMATION:
NAME: Fleit, Martin; Goll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 07/721,571
FILING DATE: 25-MAY-1990
PRIOR APPLICATION DATA:
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LENGTH: 400 residues
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   239
                                                                                                               171
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                                    227 TGMASQASETLQVPRTPRP------GVESADSR--RLATKHSRKALKAKLTLGILL 274
                                                                         183 AQECHSNPRC---CSFASNMPYALLSSSVSFYLPLLVMLFVYARVFVVAKRQR-HLLRRE 238
                                                                                                                                                                                115 LNLCLISLDRYLLILSPLRYKLRMTPLRALALYLGAWSLAALASFLPLLLGWHELG---- 170
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                                                                                                                                              ETLCALAVDRYLAVTNPLRYGTLVTKRRARAAVVLVWIVSAAVSFAPIMSQWWRVGADAE 182
                                                                                                                                                                                                                       PRIQTITNVFVTSLAAADLVVGLLVMPPGATLALTGHWPLGETGCELWTSVDVLCVTASI 122
                                                                                                                                                                                                                                                         PALRNTSNEFELVSLETSDLMVGLVVMPPAMLNALYGRWVLARGLCLLWTAEDVMCCSASI 114
LGRFSPEESPPSPSRSPSPATGGTPAAPDGVPPCGRRPARLLPLREHRALR---TLGLIM 295
                                                                                                           ----HARPPVPGQCRLLASLPFVLVASGLTFFLPSGAICFTYCRILLAARKQAVQVASLT
                                                                                                                                                                                                                                                                                              PWPHRNGSLALWSDAPTLDPSAANTSGLPGVPWAAALAGALLALATVGGNLLVIIAIART 62
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O. BOX 06110
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                                                                                                                                                                                                                                                                                                                                                                                                      Length 400;
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US-07-626-618A-21
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                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acids
TOPOLOGY: lincary
VOLECHIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Van Tol, Hubert | APPLICANT: Civelli, Olivier
                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               275
                                                              126
183 IDNCDSSLSRTYAISSSVISFYIPVAIMIVTYTRIYRIAQKQIRRIAALERAAVHAKNCQ
                             179 -- QCRLLASLPFVLVASGLTFFLPSGAICFTYCRILLAARKQAVQVASL-TTGMASQASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               356 LLCSYGGRGPEEPRAVTFPASPVEARQSPPLNRFDGYEGARP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              296 GIFSLCWLPFFLANVLRALAGPSLVPSGVFIALNWLGYANSAFNPVIYCRSPDFRDAFRR 355
                                                                                                                                67
                                                                                                                                                69 FTSDLMVGLVVMPPAMLNALYGRWVLARGLCLLWTAFDVMCCSASILNI.CLISLDRYLLI 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 312 . _ . TELEPHONE: 312-715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/
FILING DATE: 7 DEC 1990
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
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                                                                                                                                                                                                                              21 SAPGGSGWY------AAALCVVIALTAAANSLLIALICTQPALRN-TSNFFLVSL 68
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                                                                                                                               AVSDLLVAVLVMPWKAVAEIAGFWPFG-SFCNIWVAFDIMCSTASILNLCVISVDRYWAI 125
                                                                                                                                                                                               SAMDGTGLVVERDESVRILTACFLSLLILSTLLGNTLVCAAVIRERHLRSKVTNEFVISL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL----GRFLPCPRC---PRERQASLASPSLR--TSHSGPRP
                                                                                          LSPLRYKLRMTPLRALALVIGAWSLAALASFLPILLIGWHELGHARPPVPG------ 178
                                                                                                                                                                                                                                                                 143;
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10 South Wacker Drive, Suite 3000
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SYSTEM: PC-DOS/MS-DOS
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NO
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                                                                                                                                                                                                                                                                               24.18;
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                                                                                                                                                                                                                                                            79;
                                                                                                                                                                                                                                                                             Score 552.5; DB 1
Pred. No. 1.9e-34;
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                                                                                                                                                                                                                                                                 Mismatches 172;
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                                                                                                                                                                                                                                                                                             DB 1;
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                                                            -AKPTSPSDGNATSLAET · 182
                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                               Length 446;
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242
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236 TLQVPRTPRPGVESADSRRLATKHSRKALKAKLTLGILLGMFFVTWLPFFVANIVQAVCD 295

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; HYPOTHETICAL:
US-08-333-977-21
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amin -
TYPE
                                                                                                                                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/626
FILING DATE: 7 DEC 1990
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5594108nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1
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                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 312-715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
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CITY: Chicago
Illinois
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OPERATING SYSTEM:
                  69 FTSDLMVGLVVMPPAMLNALYGRWVLARGLCLLWTAFDVMCCSASILNLCLISLDRYLLI 128
                                                                                         21 SAPGGSGWV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 03-NOV-1994
                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                            Local Similarity
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                                                    SAMDGTGLVVERDESVRILTACELSLLILSTLLGNTLVCAAVIRERHLRSKVTNEFVISL 66
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10 South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                           446 amino acids
                                                                                                                               Conservative
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TBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                         ----AAALCVVIALTAAANSLLIALICTQPALRN-TSNFFLVSL 68
                                                                                                                           24.1%; Score 552.5; DB 1; 31.2%; Pred. No. 1.9e-34; tive 79; Mismatches 172;
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DB 1;
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                                                                                                                                                               Length 446;
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US-07-916-901-6
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US-07-916-901-6
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                                                                                                             TELEPHONE: (313) 689-: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                   MOLECULE TYPE:
                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rao, Donald D. TITLE OF INVENTION: @ @3
                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                    TOPOLOGY:
                                                       TYPE:
                                                                                                                                                               NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 20
CITY: Troy
                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 19920
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                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Michigan
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                                                                       LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLQVPRTPRPGVESADSRRLATKHSRKALKAKLTLGILLGMFFVTWLPFFVANIVQAVCD 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDNCDSSLSRTYAISSSVISFYIPVAIMIVTYTRIYRIAQKQIRRIAALERAAVHAKNCQ 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -- QCRLLASLPFVLVASGLTFFLPSGAICFTYCRILLAARKQAVQVASL-TTGMASQASE 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSPLRYKLRMTPLRALALVLGAWSLAALASFLPLLLGWHELGHARPPVPG----
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                                                   AMINO ACID
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                                                                                                                              (313) 689-3554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beaver - Ste. 400; P.O. Box 4390
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Query Match 24.1 Best Local Similarity 35.3 Matches 142; Conservative

24.1%; Score 551.5; DB 35.3%; Pred. No. 2e-34; Live 61; Mismatches 1

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US-07-783-602C-1
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Query Match
Best Local Similarity
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                                                                                                                                                                                NAME: J.G. NUMBER: 330/3
REGISTRATION NUMBER: 717-
REFERENCE/DOCKET NUMBER: 717-
TELECOMMUNICATION INFORMATION:
TO 103 684 1111
TO 103 684 1111
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                                                                                  TOPOLOGY: 1
MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: J. Craig Venter et al TITLE OF INVENTION: A FAT CELL SPECIFIC a-ADRENERGIC TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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                                                                    -783-602C-1
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                                                                                                                                       TYPE: /
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                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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RESULT 12
US-08-351-473B-4
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APPLICANT: LENZEN, GERLINDA
APPLICANT: KAPOOR, ARCHANA
             TELEPHONE: (703) 413-:
TELEFAX: (703) 413-22:
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                    APPLICATION NUMBER: 93 0.
FILING DATE: 21-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/1
FILING DATE: 21-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                        REFERENCE/DOCKET NUMBER: 66
TELECOMMUNICATION INFORMATION:
                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: OBLON, NORMAN F.
                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 21-FE
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC OPERATING SYSTEM:
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STATE: VIRGINIA
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                                                                                                                                 NAME: OBLON, NORMAN REGISTRATION NUMBER:
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version
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                                                                        (703) 413-3000
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TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-351-473B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-444-734A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08444734A Patent No. 5610282
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Mahan, Lawrence C. APPLICANT: McVittie, Loris D. TITLE OF INVENTION: cDNA encorrormer of INVENTION: receptor TITLE OF INVENTION: expression TITLE OF INVENTION: cell line:
PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                      CLASSIFICATION:
                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                     ZIP:
                                                                                                                                                                                                                                                                  ADDRESSEE: Knobbe, Martens, Olson and Bear STREET: 620 Newport Center Drive, Sixteenth Floor CITY: Newport Beach
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Monsma, Frederick J.
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                                                                                                                PatentIn Release #1.0, Version
                                         530
                                                                                                                                                                                                                                                                                                                                                                                           cDNA encoding the rat D1 dopamine receptor linked to adnylyl cyclase activation and expression of the receptor protein in plasmid-transfected
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RESULT 14
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                                                                                                                                         Sequence 4, Application US/07969267B Patent No. 5882855
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                                                                                     GENERAL INFORMATION:
APPLICANT: Weinshank, R:
APPLICANT: Hartig, Paul
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
FRAGMENT TYPE:
                                  TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                   CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (714) 760-0404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Altman, Daniel E. REGISTRATION NUMBER: 34,115
 ADDRESSEE:
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                                                                                                                                                                                                                                                          TPPARL
                                                                                                                                                                                                                                                                                            SSGLRL 394
                                                                                                                                                                                                                                                                                                                                AFQGLLCCARRAARRRHATHGDRPRASGCLARPG-----PPPSPGAASDDDDDDVVGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGQCRLLASLPFVLVASGLTFFLPSGAICFTYCRILLAARKQAVQVAS----LTTGMASQ 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALDRYLAITSPFRYQSLLTRARARGLVCTVWAISALVSFLPILMHWWRAESDEARRCYND 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLDRYLLILSPLRYKLRMTPLRALALVLGAWSLAALASFLPLLLGW--HELGHARPPV--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNFFLVSLFTSDLMVGLVVMPPAMLNALYGRWVLARGLCLLWTAFDVMCCSASILNLCLI 120
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                                                                                                       Weinshank, Richard L.
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Cooper & Dunham
                 ADDRESS:
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                                                 DNA Encoding
Receptor And
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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FILING DATE: 10-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Chit: The Company of 
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CLONE: D1
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                                                                                                                                                                                                                                                                                                                                                                                             243
                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 TLQVPRTPRPGVESADSRRLATKHSRKALKAKLTLGILLGMFFVTWLPFFVANIVQAVCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 IDNCDSSLSRTYAISSSVISFYIPVAIMIVTYTRIYRIAQKQIRRIAALERAAVHAKNCQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 SAPGGSGWV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                 TTTGNGKPVECSQPESSFKMSFKRETKVLK---TLSVIMGVFVCCWLPFFILNCILPFCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --QCRLLASLPFVLVASGLTFFLPSGAICFTYCRILLAARKQAVQVASL-TTGMASQASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAMDGTGLVVERDFSVRILTACFLSLLILSTLLGNTLVCAAVIRFRHLRSKVTNFFVISL
                                                                                                                                 ETVSINNNGAAMFSSHHEPRGSISKECNLVYLIPHAVGSSEDLKKEEAAGIARPLEKLSP
                                                                                                                                                                                              ----SLASPSIRTSHSGPRPGLSLQQVLPLPLPPDSDSDSDAGSGGSSGIRLTAQLLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    446 amino acids
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ALSVILDYDTDVSLEKIQPITQNGQHP 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Version
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MOLECULE TYPE:
US-08-087-772A-2
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US-08-087-772A-2
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Patent No. !
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 139; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Nanulus,
APPLICANT: Emorine, Jean L.
APPLICANT: Emorine, Jean L.
APPLICANT: Strosberg, Donny A.
APPLICANT: Strosberg, Donny A.
APPLICANT: Nucleotide Sequences Encoding
TITLE OF INVENTION: Beta3-Adrenergic Receptor and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS: LENGTH: 388 amino acids
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NAME: Linker, Raymond O.
REGISTRATION NUMBER: 26,
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: 919-881-3140
   330
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CLASSIFICATION:
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ALGRFLPCP---RCPRERQASL--ASP 351
                                   GIFSLCWLPFFLANVLRALAGPSLVPSGVFIALNWLGYANSAFNPVIYCRSP----DFRD
                                                                 GMFFVTWLPFFVANIVQAVC--DCISPGLFDVLTWLGYCNSTMNPIIY---PLFMRDFKR 329
                                                                                                     LGRFSPEESPPSPSRSPSPATGGTPAAPDGVPPCGRRPARLLPLREHRALR---TLGLIM
                                                                                                                                                                        AQECHSNPRC---CSFASNMPYALLSSSVSFYLPLLVMLFVYARVFVVAKRQR-HLLRRE
                                                                                                                                                                                                                                                                                                            PRIQTITNVFVTSLAAADLVVGLIVMPPGATLALTGHWPLGETGCELWTSVDVLCVTASI 122
                                                                                                                                                                                                                                                                                                                                                                               PWPHRNGSLALWSDAPTLDPSAANTSGLPGVPWAAALAGALLALATVGGNLLVIIAIART 62
                                                                                                                                                                                                                                                                                                                                                                                                             PGPTANSTPA-WGAGP---PSAPGGSG----WVAAALCVVIAL-TAAANSLLIALICTQ 54
                                                                                                                                     TGMASQASETLQVPRTPRP------GVESADSR--RLATKHSRKALKAKLTLGILL
                                                                                                                                                                                                        ----HARPPVPGQCRLLASLPFVLVASGLTFFLPSGAICFTYCRILLAARKQAVQVASLT
                                                                                                                                                                                                                                            ETLCALAVDRYLAVTNPLRYGTLVTKRRARAAVVLVWIVSAAVSFAP1MSQWWRVGADAE
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: No. 5691155th Carolina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.8%; Score 546; DB 1 35.9%; Pred. No. 5e-34;
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, Db 352 AFRRLL-CSYGGRGPEEPRAVTFPASP 377

Search completed: March 15, 2002, 14:10:25 Job time: 115 sec .